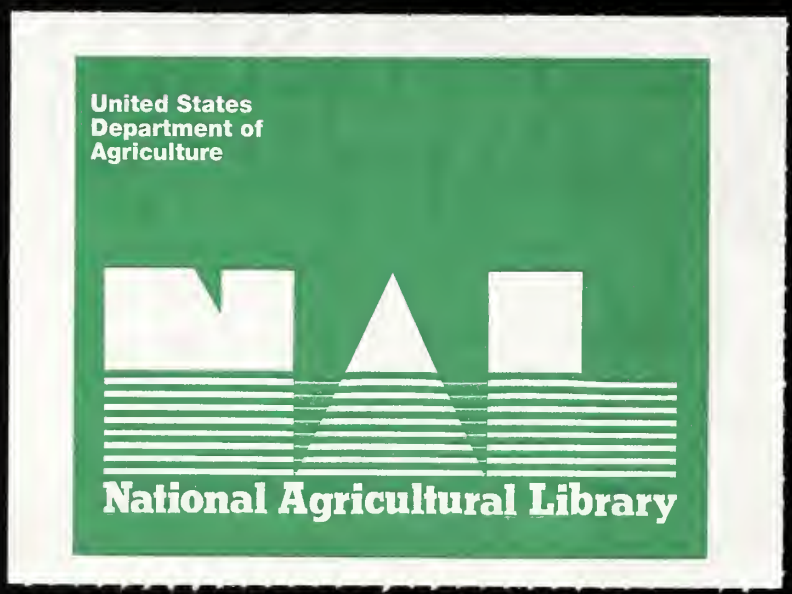
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Draft Risk Assessment of the Public Health Impact of *Escherichia coli* O157:H7 in Ground Beef

Prepared for the Food Safety and Inspection Service by the *Escherichia coli* O157:H7 Risk Assessment Team

FSIS

List of Contributors to the *Escherichia coli* O157:H7 Risk Assessment

This U.S. Department of Agriculture, Food Safety and Inspection Service draft risk assessment was developed with contributions from the following organizations:

- U.S. Department of Agriculture, Food Safety and Inspection Service
- U.S. Department of Agriculture, Economic Research Service
- U.S. Department of Health and Human Services, Food and Drug Administration
- U.S. Department of Health and Human Services, Centers for Disease Control and Prevention
- National Advisory Committee on Microbiological Criteria for Foods
- Interagency Food Risk Assessment Group
- North Carolina State University
- University of Delaware
- University of Maryland
- David Vose Risk Services
- University of Tasmania

The *E. coli* O157:H7 draft risk assessment has been reviewed by individuals chosen from these organizations for their diverse perspectives and technical expertise. The purpose of this review was to provide candid and critical comments that will assist the Food Safety and Inspection Service in developing a scientifically sound risk assessment. The review comments and draft manuscripts remain confidential to protect the integrity of the deliberative process.

The organizations listed above have provided many constructive comments and suggestions. It must be emphasized, however, that responsibility for the final content of this report rests entirely with the U.S. Department of Agriculture, Food Safety and Inspection Service.

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Executive Summary

The Office of Public Health and Science (OPHS) in the U.S. Department of Agriculture's Food Safety and Inspection Service (USDA/FSIS) conducted a farm-to-table risk assessment to evaluate the public health impact from *Escherichia coli* O157:H7 in ground beef. This risk assessment was initiated in response to the identification of *E. coli* O157:H7 in cattle, on carcasses, and in ground beef, as well as heightened public awareness of the association of *E. coli* O157:H7 with foodborne outbreaks that have resulted in severe illness and death. The purpose of this risk assessment is to systematically evaluate and integrate available scientific data and information to

- provide a comprehensive evaluation of the risk of illness from *E. coli* O157:H7 in ground beef based on currently available data,
- estimate the likelihood of human morbidity and mortality associated with specific numbers of *E. coli* O157:H7 in ground beef servings,
- estimate the occurrence and extent of *E. coli* O157:H7 contamination at points along the farm-to-table continuum,
- provide a tool for analyzing how to most effectively mitigate the risk of illness from *E. coli* O157:H7 in ground beef (one that is useful for Pathogen Reduction and Hazard Analysis and Critical Control Point applications),
- identify future food safety research needs, and
- assist FSIS in the review and refinement of its integrated risk reduction strategy for *E. coli* O157:H7 in ground beef.

BACKGROUND

E. coli O157:H7 was first recognized as a foodborne pathogen with major public health consequences in 1982, when it was associated with two outbreaks of bloody diarrhea in Oregon and Michigan. An estimated 62,000 cases of symptomatic *E. coli* O157:H7 infections occur annually in the United States due to foodborne exposures, resulting in approximately 1,800 hospitalizations and 52 deaths. As many as 3,000 cases may develop hemolytic uremic syndrome annually. Surveillance data indicate that the highest incidence of illness from *E. coli* O157:H7 occurs in children under 5 years of age.

Epidemiological evidence indicates that ground beef is a primary source of human exposure to *E. coli* O157:H7. Between 1982 and 1993, ground beef was identified as the transmission source in 54% of *E. coli* O157:H7 outbreaks. Of the *E. coli* O157:H7 outbreaks reported between 1993 and 1998, most (72%) were foodborne. Of the foods implicated in these outbreaks, ground beef was the most common (45%) source. Studies of sporadic cases of *E. coli* O157:H7 illness also identified ground beef as the primary source of human exposure.

As the public health regulatory agency responsible for ensuring that meat and poultry products are properly labeled, wholesome, and safe, FSIS took additional steps to prevent the occurrence of *E. coli* O157:H7 in ground beef sold to the U.S. public, including improving its sampling and detection methods for *E. coli* O157:H7 in ground beef, strengthening consumer education initiatives that are focused on proper cooking and handling of ground beef, and setting policy declaring *E. coli* O157:H7 in raw ground beef an adulterant. On August 18, 1998, FSIS announced plans to develop the farm-to-table risk assessment documented in this report.

STRUCTURE AND SCOPE OF THE *E. COLI* O157:H7 RISK ASSESSMENT

The *E. coli* O157:H7 risk assessment is a *baseline* risk assessment in that it reflects, to the extent practicable, a full range of current practices, behaviors, and conditions in the farm-to-table continuum (production, slaughter, processing, transportation, storage, preparation, and consumption) (Figure ES-1). Scientific data and information available through July 2001 were integrated into the generally accepted framework for microbiological risk assessments: hazard identification (Chapter 2), exposure assessment (Chapter 3), hazard characterization (Chapter 4), and risk characterization (Chapter 5). Each component of the assessment has a distinct role.

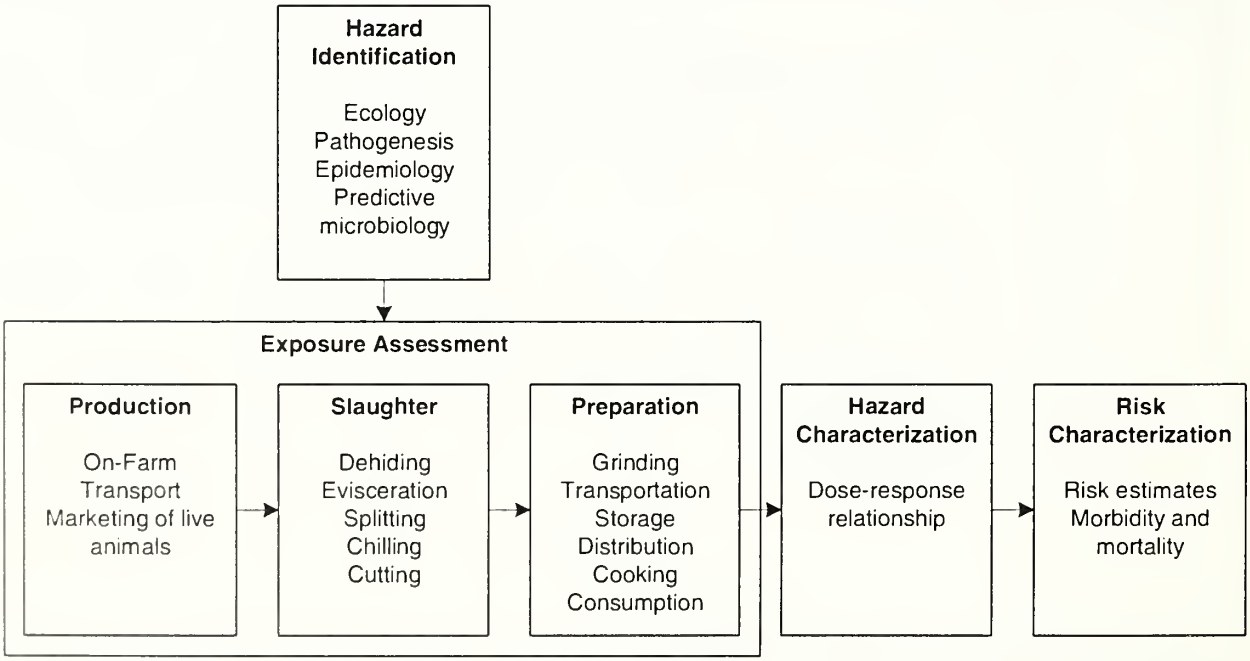

FIGURE ES-1 Farm-to-table risk assessment model for *E. coli* O157:H7 in ground beef.

Hazard identification characterizes *E. coli* O157:H7 using data from ecology, pathology, epidemiology, and microbiology.

Exposure assessment comprises three modules—production, slaughter, and preparation—and uses probabilistic techniques to model the prevalence and concentration of *E. coli* O157:H7 in live cattle, carcasses, beef trim, and, ultimately, a single serving of cooked ground beef. Data for the exposure assessment include herd and within-herd prevalence of *E. coli* O157:H7, slaughter processing conditions including decontamination steps, consumer and retail storage and cooking behaviors contributing to the growth or decline in the number of *E. coli* O157:H7 organisms in ground beef servings, and consumer demographics (e.g., age of the consumer and location of the meal) and consumption patterns. Seasonal differences in herd prevalence of *E. coli* O157:H7 infection were also included.

Hazard characterization quantifies the nature and severity of the adverse health effects (i.e., illness or death) (response) associated with exposure to a given number of *E. coli* O157:H7 organisms in a ground beef serving (dose). For *E. coli* O157:H7, the precise relationship between the number of organisms consumed and the resulting adverse human health event is not known. The *E. coli* O157:H7 dose-response function was derived using information from three sources: (1) the estimated annual number of symptomatic *E. coli* O157:H7 infections due to ground beef exposure, (2) the estimated number of contaminated ground beef servings from the exposure assessment, and (3) the lower and upper bound dose-response curves derived using surrogate pathogens. The upper and lower bound dose-response curves describe the uncertainty about the probability of symptomatic illness at an ingested dose (the median *E. coli* O157:H7 dose-response function). Seasonal variability in reported *E. coli* O157:H7 cases was also included.

Risk characterization integrates the results of the exposure assessment and hazard characterization to estimate the risk of illness from *E. coli* O157:H7 in ground beef. Risk estimates are provided for individuals, a community in a simulated outbreak scenario, and the U.S. population. The variability of risk among the U.S. population is considered according to differences in seasonal exposure and host susceptibility (based on the age of the consumer). Also included in the risk characterization is a sensitivity analysis to identify factors that most influence the occurrence and number of *E. coli* O157:H7 organisms in ground beef and the subsequent risk of illness. Factors that most influence the risk of illness, but for which there were limited data and information, are identified as important food safety research areas.

As announced in the *Federal Register* (Volume 63, page 44232), this risk assessment is confined to *E. coli* O157:H7 exposure from the consumption of ground beef servings (e.g., hamburgers, meat balls, and meat loaf) in the United States. Only *E. coli* O157:H7 generated from infected cattle and subsequent contaminated beef trim and ground beef were considered. Exposures from cross-contamination or other sources of *E. coli* O157:H7 (e.g., nonground beef foods, water, and fomites) were outside the scope of this assessment. This risk assessment also does not explicitly model imported beef as distinct from domestic beef. However, seasonal variation in the incidence of *E. coli* O157:H7 infection in U.S. cattle and human population is included.

RESULTS OF THE *E. COLI* O157:H7 RISK ASSESSMENT

The risk assessment yields intermediate and final outputs in the form of distributions that characterize the variability and uncertainty in estimates of a variety of risk assessment endpoints or human illnesses. The exposure assessment indicates that feedlot cattle (steers and heifers) have a higher prevalence of *E. coli* O157:H7 infection than culled breeding cattle (cows and bulls) and that prevalence is higher during June to September than October to May. Although only a fraction of infected live cattle result in contaminated carcasses, thousands of pounds of meat trim from these carcasses are combined in the grinding process. Consequently, although the

number of *E. coli* O157:H7 organisms in these grinder loads may be quite low, the proportion of grinder loads that contain at least 1 *E. coli* O157:H7 organism is expected to be high. Most ground beef servings are cooked in the United States. Less than 0.007% to 0.018% (depending on seasonal exposure) of cooked ground beef servings contain *E. coli* O157:H7 organisms. However, considerable uncertainty exists regarding the frequency of cooked ground beef servings that have 1 or more *E. coli* O157:H7 present.

The median probability of illness for the general U.S. population due to *E. coli* O157:H7 from a serving of ground beef is estimated to be 9.6×10^{-07} or about 1 illness in every 1 million servings. Based on a U.S. population risk of illness from *E. coli* O157:H7-contaminated ground beef, the per serving probability of being hospitalized but recovering is 2.0×10^{-8}, of developing HUS is 4.2×10^{-9}, and of death is 5.9×10^{-10}. When variation in seasonal exposure is considered, the risk of illness from *E. coli* O157:H7 is about 1 in every 600,000 ground beef servings consumed during June through September and about 1 in every 1.6 million ground beef servings consumed during October through May. Children aged 0 to 5 may have an almost 2.5 times higher risk of illness (2.4×10^{-6}) from *E. coli* O157:H7 in ground beef than does the general U.S. population.

Factors that most influence the occurrence and extent of *E. coli* O157:H7 contamination in ground beef and subsequent risk of illness were identified using sensitivity analyses. The occurrence and extent of *E. coli* O157:H7 contamination in beef trim and subsequent grinder loads was most influenced by feedlot and within-feedlot prevalence, occurrence and extent of carcass contamination, effectiveness of decontamination procedures, and the effect of carcass chilling. The occurrence and extent of *E. coli* O157:H7 contamination in cooked ground beef servings was most influenced by the proportion of ground beef that was frozen, the maximum *E. coli* O157:H7 population density in ground beef servings, and storage and cooking conditions. The importance of these factors varied by season (June to September or October to May). Although some factors influenced the occurrence of *E. coli* O157:H7 in combo bins, grinder loads, or ground beef servings, others were more important in influencing the extent of *E. coli* O157:H7 contamination in these units.

RESEARCH NEEDS

The *E. coli* O157:H7 risk assessment is structured to allow incorporation of additional data as they become available. The determination of which data would be most beneficial is based on areas identified as important and for which there is limited information. Several areas of food safety research would strengthen the certainty of estimates from this risk assessment, including

- additional information on *E. coli* O157:H7 contamination of cattle and carcasses following dehiding;
- data on the effect of carcass chilling on increases or decreases in *E. coli* O157:H7 organisms;
- predictive microbiological data on the increase and decrease in the number of *E. coli* O157:H7 organisms in ground beef under various storage and preparation conditions along with estimates of the frequencies of occurrence of these storage and preparation conditions;

- information on the maximum density of *E. coli* O157:H7 organisms in ground beef servings as a result of matrix effects, competitive microflora in ground beef, and environmental conditions (e.g., pH, water activity); and
- Data on retail (hotels, restaurants, and institutions [HRI]) and consumer storage, cooking, and consumption (frequency and serving size) patterns by type of ground beef meal (e.g., grilled hamburger or baked meat loaf) and season.

NEXT STEPS

Some cautions on the appropriate use of this risk assessment should be noted. First, the conclusions are based on current data and scientific assumptions. Additional data will be incorporated into the model as they become available. Second, the results provide only part of the information needed by decision makers and regulators. This risk assessment does not address such issues as cost, feasibility, or effectiveness of possible interventions. These analyses are necessary before deciding which of many possible policies should be implemented regarding *E. coli* O157:H7 in ground beef.

Future plans for this risk assessment include evaluating the effect that various mitigation strategies may have in decreasing the occurrence of *E. coli* O157:H7 in ground beef and associated human illnesses. FSIS also plans to expand the risk assessment to include other beef products (i.e., nonintact beef).

FSIS is releasing this draft report documenting the baseline risk assessment on *E. coli* O157:H7 in ground beef for public comment and scientific peer review by the National Academy of Sciences. Thus, the risk assessment is a "work in progress." FSIS invites public input to further strengthen this farm-to-table baseline risk assessment for *E. coli* O157:H7 in ground beef.

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Introduction

Escherichia coli O157:H7 was first recognized as a foodborne pathogen with major public health consequences in 1982, when it was associated with two outbreaks of bloody diarrhea in Oregon and Michigan (Riley et al. 1983). Between 1982 and 1998, over 4,400 cases of human illness resulted from 203 outbreaks that involved exposure to *E. coli* O157:H7 (CDC unpublished data). Of these cases, 968 (22%) were hospitalized, 228 (5%) progressed to hemolytic uremic syndrome (HUS) or thrombotic thrombocytopenic purpura (TTP), and 28 (0.6%) died. Surveillance data indicate that the highest incidence of illness from *E. coli* O157:H7 occurs in children under 5 years of age (CDC 1999a).

Epidemiological evidence indicates that ground beef is the primary source of human exposure to *E. coli* O157:H7. Between 1982 and 1993, ground beef was identified as the transmission source in 54% of *E. coli* O157:H7 outbreaks (Griffin 1995). Of the *E. coli* O157:H7 outbreaks reported between 1993 and 1998, most (72%) were foodborne. Of the foods implicated in these outbreaks, beef was the most common (45%) source. When specified, 90% of the time the beef product was ground (CDC 1999b; CDC 2000; CDC 2001). Studies of sporadic cases of *E. coli* O157:H7 illness also identified ground beef as the primary source of human exposure (MacDonald et al. 1988; Le Saux et al. 1993; Mead et al. 1997; Slutsker et al. 1998; Kassenborg et al. 2001).

As the public health regulatory agency responsible for ensuring that meat and poultry products are properly labeled, wholesome, and safe, the Food Safety and Inspection Service (FSIS) took the following additional steps to prevent the occurrence of *E. coli* O157:H7 in ground beef sold to the U.S. public:

- In August 1994, FSIS declared that ground beef containing *E. coli* O157:H7 is adulterated under the Federal Meat Inspection Act unless further processed in a manner that destroys this pathogen.[1]
- On October 17, 1994, FSIS initiated a microbiological testing program for *E. coli* O157:H7 in raw ground beef in meat plants and retail stores.[2] The initial testing program was established and designed to test approximately 5,000 raw ground beef samples per year, 50% from federally inspected plants and 50% from retail stores.
- In 1998, because of the low concentrations of *E. coli* O157:H7 recovered from samples of frozen ground beef patties identified in 1993 and 1997 *E. coli* O157:H7 outbreaks in Colorado[3,4], FSIS increased the microbiological testing sample size from 25 grams to 325 grams. The increased sample sizes were necessary to improve detection of *E. coli* O157:H7 in raw ground beef sold to consumers.
- In August 1998, FSIS initiated a consumer education campaign encouraging use of food thermometers to ensure that ground beef is cooked to an internal temperature of at least 160°F (FSIS 1998).
- In September 1999, FSIS introduced a more sensitive laboratory test for *E. coli* O157:H7 that used an additional selective capture step based on immunomagnetic separation (FSIS 1999).[5]
- In February 1999, FSIS proposed to permit the use of ionizing radiation for treating refrigerated or frozen uncooked meat food products to reduce the concentration of foodborne pathogens, including *E. coli* O157:H7 (*Federal Register*, Volume 64, pages 9089-9105).[6]

PURPOSE OF THE *E. COLI* O157:H7 RISK ASSESSMENT

In addition to setting new standards and improving microbiological testing for *E. coli* O157:H7 in ground beef, on August 18, 1998, FSIS announced plans to conduct a farm-to-table risk assessment (*Federal Register*, Volume 63, page 44232). The result was the risk assessment documented in this report. The overall goals of this risk assessment are to

- provide a comprehensive evaluation of the risk of illness from *E. coli* O157:H7 in ground beef based on currently available scientific data,
- estimate the likelihood of human morbidity and mortality associated with specific numbers of *E. coli* O157:H7 in ground beef servings,

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[1]If a ground beef sample is confirmed positive, FSIS inspectors will condemn the sampled lot unless it is fully cooked (in accordance with 9 CFR 318.23) or processed in a way that would eliminate the pathogen (FSIS Directive 10,010.1). FSIS Directive 8080.1 Rev. 2 (11-3-92) outlines the basic procedures for recall of an inspected meat or poultry product.

[2]In December 1994, the agency won a court challenge of the policy and the testing program. The testing program operated under FSIS Notice 50-94, issued on December 23, 1994, until the agency issued FSIS Directive 10,010.1 on February 1, 1998.

[3]The most probable number (MPN) of *E. coli* O157:H7 recovered from six samples from the 1993 outbreak ranged from 30 to 1,500 organisms per 100 grams (Johnson et al. 1995; Marks et al. 1998).

[4]Tuttle et al. (1999) reported an MPN of 67 *E. coli* O157:H7 organisms per uncooked patty.

[5]Consequently, recent increases in the reported frequency of *E. coli* O157:H7 detection reflect, at least in part, increased sample sizes and the use of a more sensitive test for detection of *E. coli* O157:H7.

[6]The Final Rule for the Irradiation of Meat Food Products was published on December 23, 1999 (*Federal Register*, Volume 64, pages 72149-72166).

- estimate the occurrence and extent of *E. coli* O157:H7 contamination at points along the farm-to-table continuum,
- provide a tool for analyzing how to most effectively mitigate the risk of illness from *E. coli* O157:H7 in ground beef (one that is useful for Pathogen Reduction and Hazard Analysis and Critical Control Point applications),
- identify future food safety research needs, and
- assist FSIS in the review and refinement of its integrated risk reduction strategy for *E. coli* O157:H7 in ground beef.

STRUCTURE OF THE *E. COLI* O157:H7 RISK ASSESSMENT

The *E. coli* O157:H7 risk assessment follows the generally accepted structure for microbiological risk assessments: hazard identification, exposure assessment, hazard characterization, and risk characterization. *Hazard identification* serves to identify biological agents that may be present in a particular food or groups of food and are capable of causing adverse health effects. *Exposure assessment* is the quantitative evaluation of the likely intake of biological agents via food, as well as exposures from other sources, if relevant. *Hazard characterization* is the quantitative evaluation of the adverse health effects associated with the hazard. This step includes a *dose-response assessment* that determines the relationship between the magnitude of exposure dose to a biological agent and the frequency of associated adverse health effects (response). Finally, *risk characterization* is the process of determining the quantitative estimation, including attendant uncertainties, of the frequency of occurrence and severity of adverse health effects in a given population based on the hazard identification, exposure assessment, and hazard characterization.

The *E. coli* O157:H7 risk assessment provides numerical expressions of risk and an indication of the attendant uncertainties. Scientific data are the foundation of this risk assessment. This risk assessment includes data available through July 2001. By integrating scientific data through a structured process, the *E. coli* O157:H7 risk assessment provides information that links policy and science. A structured process is essential to risk assessment because describing risk rarely involves the certainty of direct, measurable observations relevant to human health; instead, it involves statistical estimation and prediction, as well as transparent expression of uncertainty.

The *E. coli* O157:H7 risk assessment is a *baseline* risk assessment in that it reflects, to the extent practicable, a full range of current practices, behaviors, and conditions in the farm-to-table continuum (production, slaughter, processing, transportation, storage, preparation, and consumption) (Figure 1-1). This risk assessment is intended to assist FSIS risk managers in identifying potential areas along the farm-to-table continuum to control *E. coli* O157:H7. Using this baseline risk assessment, risk managers will identify a set of feasible control options to analyze. Use of the risk assessment to evaluate different control strategies is known as conducting a scenario analysis. Subsequent scenario analyses using the *E. coli* O157:H7 risk assessment will provide FSIS decision makers with information concerning the efficacy of alternative mitigation strategies and a tool to evaluate these strategies to decrease the number of human illnesses resulting from *E. coli* O157:H7 in ground beef. A sensitivity analysis is included with this baseline risk assessment to provide FSIS risk managers with information on (1) the potential areas to consider in reviewing and refining mitigation strategies and (2) the most important data gaps and key uncertainties for future data collection and research.

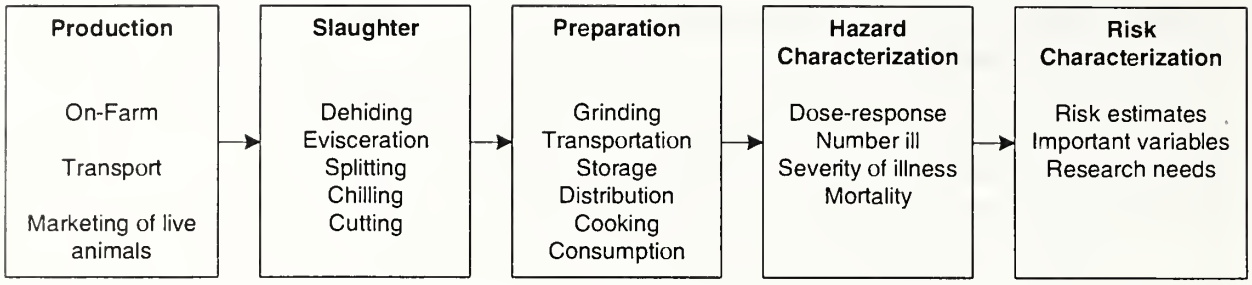

FIGURE 1-1 Risk assessment structure for *E. coli* O157:H7 in ground beef.

SCOPE OF THE *E. COLI* O157:H7 RISK ASSESSMENT

As announced in the *Federal Register* (Volume 63, page 44232), the scope of this risk assessment is confined to ground beef products, based on an analysis of available epidemiologic data (Mead et al. 1999).[7] At the broadest level of aggregation, the scope of the assessment includes two classes of product: (1) products consisting of 100% ground beef and (2) other products containing ground beef. Due to the lack of available data, the scope of the assessment does not distinguish ground beef products (i.e., hamburger or meat patties [as defined in 9 CFR 319.15] that also contain comminuted beef processed by means other than grinding [e.g., mechanical separation and partial defatting])

A number of factors were considered in assessing the risk of illness from *E. coli* O157:H7 in ground beef, including (1) the number of illnesses and severity of these illnesses caused by *E. coli* O157:H in ground beef; (2) the likelihood of *E. coli* O157:H7 (hazard) being present in a ground beef serving (exposure); (3) the likelihood that exposure to a given number of *E. coli* O157:H7 in a ground beef serving will cause illness (dose-response); (4) the probability of illness from *E. coli* O157:H7 in ground beef servings (risk); (5) consideration of the risk of illness from several perspectives (individual, community, and population); (6) the variation in population exposure (e.g., seasonal exposure) and response (e.g., by age category, children under 5 years of age) (variability); (7) identification of production, slaughter, and preparation practices and conditions that influence the likelihood of exposure to *E. coli* O157:H7 in ground beef or the subsequent risk of illness (sensitivity analysis); and (8) limitations in the current state of knowledge (uncertainty).

Beyond the scope of the present risk assessment are nonintact cuts of beef in which *E. coli* O157:H7 may be introduced below the surface of the whole cut. This may occur by means of injection, mechanical tenderizing, or reconstruction (e.g., beef that has been scored to incorporate a marinade or that has been cubed and mechanically tenderized, and restructured beef products such as gyros). Contamination may also occur in a comminution process such as chopping, flaking, or mincing (e.g., fresh veal sausage and fabricated beefsteak) the whole cut. If, however, such a comminuted beef product is combined with ground beef in the formulation of

[7]On January 19, 1999, FSIS announced that, in addition to ground beef, beef trimmings defined as intact are considered adulterated if they contain *E. coli* O157:H7. FSIS said resulting processed products from the contaminated trimmings are considered adulterated and must not be distributed until they have been processed into a ready-to-eat product (i.e., a food product that may be consumed safely without any further cooking or other preparation) (*Federal Register*, Volume 64, pages 2803-2805). For a discussion of more recent developments regarding FSIS policy for beef products contaminated with *E. coli* O157:H7, see the *Federal Register*, Volume 65, pages 6881-6886.

a food product, it is included in the scope of this risk assessment. FSIS plans to incorporate nonintact beef products that are beyond the scope of the present assessment in future iterations of this risk assessment model.

This risk assessment also does not explicitly model imported beef as distinct from domestic beef. Approximately 15% of the fresh, chilled, and frozen beef and veal consumed in the United States originates from outside the country, and 90% of such imports are from Australia, New Zealand, and Canada (APHIS:VS:CEAH 1994). Specific data regarding the prevalence of *E. coli* O157:H7 in beef imported from various countries are lacking, and published surveillance data from the three major exporters to the U.S. are variable. However, evidence does indicate that *E. coli* O157:H7 occurs in Australian, New Zealand, and Canadian cattle and humans (Robins–Browne et al. 1998; New Zealand Public Health Report 2000; Spika et al. 1998). In general, this evidence does not suggest that the prevalence of *E. coli* O157:H7 is dramatically greater in those countries than in the United States. Therefore, the assumption of equivalence in contamination of imported and domestic product is likely conservative in the model.

As announced in the *Federal Register* (Volume 63, page 44232), the scope of the analysis does not extend beyond beef as a vehicle of infection. A common concern expressed in public comments submitted to the docket and during the October 28, 1998, public meeting was that the proposed scope of the analysis was limited to foods containing ground beef and thereby omitted other important sources of *E. coli* O157:H7 infection, such as vegetables, produce, juice, water, and person-to-person transmission. However, FSIS determined that to make the analysis tractable, and in light of resource and time constraints, the scope of the assessment would necessarily have to be fixed or defined. Furthermore, the Centers for Disease Control and Prevention (CDC) recently estimated the total disease burden of *E. coli* O157:H7 from all products based on epidemiologic surveillance data (Mead et al. 1999). Consequently, there has been no attempt to quantitatively model cross-contamination or other sources of *E. coli* O157:H7 (e.g., nonbeef food products, water, and fomites). Similarly, there are currently no plans to quantitatively model secondary infections resulting from person-to-person contact. The delimited scope of the analysis has been taken into account in comparing the results predicted by the baseline risk assessment model with estimates of illnesses derived from observed epidemiologic data (Mead et al. 1999).

An increased seasonal incidence of *E. coli* O157:H7 infections in U.S. cattle and human populations has been previously demonstrated in the warm months (i.e., June to September) (Hancock et al. 1997a, 1997b; Griffin 1998). Seasonal patterns are also demonstrated for Canada (Van Donkersgoed et al. 1997) and likely occur in other countries. Seasonal effects were modeled in this risk assessment using data on the prevalence of *E. coli* O157:H7 within infected cattle herds. To improve the certainty of modeling seasonal variability for the risk of illness from *E. coli* O157:H7, additional data are needed on changes in the occurrence of *E. coli* O157:H7 in raw ground beef across seasons; changes in slaughter and processing practices by season; and changes in storage, handling, preparation, and consumption practices by season.

RESULTS OF THE *E. COLI* O157:H7 RISK ASSESSMENT

The risk assessment model yields intermediate and final outputs in the form of distributions that characterize the variability and uncertainty in estimates of a variety of risk assessment endpoints or human illnesses (Table 1-1). For hazard identification, outputs include information on the

TABLE 1-1 Outputs of the *E. coli* O157:H7 Risk Assessment

Component	Module	Outputs
Hazard Identification		Epidemiological information on human morbidity and mortality due to *E. coli* O157:H7
		Microbiological information on the pathogenesis of *E. coli* O157:H7 compared with other *E. coli* strains
		Information on the source and transmission of *E. coli* O157:H7
		Information on the environmental conditions that influence survival and growth (predictive microbiology) of *E. coli* O157:H7
Exposure Assessment	Production	Herd and within-herd prevalence rates for infected live cattle prior to slaughter for ground beef
		Prevalence of contaminated carcasses
	Slaughter	Number of *E. coli* O157:H7 organisms on contaminated carcasses
		Prevalence of contaminated combo bins of trim
		Number of *E. coli* O157:H7 organisms in combo bins of contaminated trim
		Prevalence of contaminated grinder loads of ground product
	Preparation	Number of *E. coli* O157:H7 organisms in contaminated grinder loads of ground product
		Prevalence of contaminated cooked ground beef servings
		Number of *E. coli* O157:H7 organisms in contaminated cooked ground beef servings
Hazard Characterization		Annual number of *E. coli* O157:H7 illnesses associated with cooked ground beef consumption
		Annual number of hospitalizations due to *E. coli* O157:H7 in cooked ground beef
		Annual number of cases of HUS/TTP due to *E. coli* O157:H7 in cooked ground beef
		Annual number of deaths due to *E. coli* O157:H7 in cooked ground beef
Risk Characterization		Annual risk of illness from *E. coli* O157:H7 in cooked ground beef
		Annual risk of illness from *E. coli* O157:H7 in cooked ground beef by seasonal exposure and age of the consumer
		Identification of important variables that influence the risk of illness from *E. coli* O157:H7 in ground beef
		Identification of important food safety research areas

epidemiology, transmission, ecology, and pathogenesis of *E. coli* O157:H7. Exposure assessment outputs include the prevalence of *E. coli* O157:H7-infected cattle and the occurrence and number of *E. coli* O157:H7 in combo bins of beef trim, grinder loads of ground beef, and cooked ground beef servings. Primary outputs of the hazard characterization are the number and severity of human illnesses associated with a specific number of *E. coli* O157:H7 organisms per serving (dose) and a derived dose-response function. Final outputs of the risk assessment are provided in the risk characterization and include (1) estimates of the risk of illness from *E. coli* O157:H7-contaminated ground beef for individuals, communities, and the U.S. population; (2) estimates of the U.S. population risk by season (June to September and May to October) and age (i.e., children under 5 years of age); (3) estimates of variables that are most responsible for influencing the likelihood of exposure to *E. coli* O157:H7 in ground beef servings and subsequent risk of illness; and (4) identification of important food safety research needs.

HISTORY OF THE *E. COLI* O157:H7 RISK ASSESSMENT PROJECT

Work on the *E. coli* O157:H7 baseline risk assessment in ground beef was initiated in March 1998 when the Interagency Food Risk Assessment Group, convened by the Office of Risk Assessment and Cost Benefit Analysis, formed an informal resource group. This interagency group identified resources and available data to initiate this risk assessment and organized a public meeting to solicit comment and input at an early stage of this project about the

- scope of the risk assessment,
- analytical framework to be used in conducting the risk assessment,
- scientific evidence acquired by the risk assessment team to date, and
- existing data gaps identified by the risk assessment team.

The public meeting was held on October 28, 1998, in Arlington, Virginia, and was attended by more than 60 individuals. At this meeting, FSIS released the "Preliminary Pathways and Data for a Risk Assessment of *E. coli* O157:H7 in Beef." That document summarized the currently available data and potential foodborne exposure pathways under consideration for this risk assessment.

Comments and additional data identified during the public meeting or submitted to the docket in response to the August 18, 1998, *Federal Register* Notice were evaluated for inclusion in the development of the baseline risk assessment. A complete transcript of the public meeting and all public submissions regarding the risk assessment are on file in the FSIS docket (Docket Number 98-037N, U.S. Department of Agriculture, Food Safety and Inspection Service, Room 102, 300 12th Street, SW, Washington, DC 20250-3700).

An interim draft of the *E. coli* O157:H7 baseline risk assessment was presented for public and scientific input at several meetings, including the 1998 Annual Meeting of the Society for Risk Analysis (SRA); the 1999 Annual Meeting of the International Association of Milk, Food and Environmental Sanitarians; a week-long interagency workshop on microbial risk held in April 1999; the 1999 Annual Meeting of the SRA; and the National Advisory Committee on Microbiological Criteria for Foods (NACMCF). A revised interim draft *E. coli* O157:H7 baseline risk assessment report incorporating public and scientific input from these meetings was developed. This interim draft report was presented to the public on February 29, 2000, to discuss FSIS policy regarding *E. coli* O157:H7. The presentation is available at http://www.fsis.usda.gov/OPHS/ecolrisk.

Based on input from these meetings, this risk assessment has been substantially revised and strengthened. FSIS is releasing this draft report documenting the baseline risk assessment on *E.*

coli O157:H7 in ground beef for public comment and scientific peer review by the National Academy of Sciences. This risk assessment is a "work in progress." In finalizing the baseline *E. coli* O157:H7 risk assessment, the agency will consider the comments of the National Academy of Sciences and public comments submitted to the FSIS docket within 60 days of the release date of this report.

ORGANIZATION OF THE REMAINDER OF THIS REPORT

This risk assessment report is divided into five chapters. Chapter 2 (hazard identification) provides information on the epidemiology, pathogenesis, transmission, and ecology of *E. coli* O157:H7. Chapter 3 (exposure assessment) describes the occurrence and number of *E. coli* O157:H7 organisms from farm to table. Chapter 4 (hazard characterization) discusses the derivation of a dose-response function for *E. coli* O157:H7. Chapter 5 (risk characterization) integrates the results of the previous chapters to provide estimates of the risk of illness from *E. coli* O157:H7 in ground beef. Risk characterization also includes a sensitivity analysis, identifying variables along the farm-to-table continuum that greatly influence the risk of illness from *E. coli* O157:H7. Variables that are identified as important but for which there is limited information are listed as areas for further research in Chapter 5.

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2

Hazard Identification

Escherichia coli O157:H7, a Shiga toxin-producing *E. coli,* was first recognized as a human pathogen in 1982, when it was associated with two outbreaks of hemorrhagic colitis (bloody diarrhea). The outbreaks occurred in Oregon and Michigan and involved the consumption of hamburgers from a fast-food chain (Riley et al. 1983). The spectrum of infection with *E. coli* O157:H7 includes asymptomatic fecal shedding of the organism; nonbloody or bloody diarrhea accompanied by abdominal cramps, vomiting, and occasionally fever; postdiarrheal hemolytic uremic syndrome (HUS); and thrombotic thrombocytopenic purpura (TTP). The continued occurrence of widespread outbreaks and an increase in the incidence of reported cases have led to the designation of *E. coli* O157:H7 as an emerging pathogen. Since 1982, epidemiologic studies have shown that *E. coli* O157:H7 can be transmitted through water (by drinking or swimming in contaminated water), food, or person-to-person contact, especially in a daycare setting. Ground beef continues to be a significant source of *E. coli* O157:H7 infection in humans. This chapter on hazard identification begins with a discussion of the importance of *E. coli* O157:H7 in the context of other Shiga toxin-producing *E. coli*. The chapter then discusses the sources of *E. coli* O157:H7; its epidemiology, including the types of food and risk factors associated with infection; adverse health outcomes; and the organism's pathogenesis. The factors that contribute to the growth and persistence of *E. coli* O157:H7 in the environment are then discussed.

ESCHERICHIA COLI

Multiple genetic subtypes of *E. coli* exist; many are part of the normal mammalian intestinal flora and do not cause disease in humans. *E. coli* strains that cause diarrheal illness are categorized into specific groups on the basis of virulence properties, mechanisms of pathogenicity, and clinical syndromes. These categories include enteropathogenic *E. coli* (EPEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), diffuse-adhering *E. coli* (DAEC), enteroaggregative *E. coli* (EaggEC), and Shiga toxin-producing *E. coli* (STEC). *E. coli*

O157:H7 is in the STEC group and can produce Shiga toxin 1, Shiga toxin 2, or both. Shiga toxin production alone may not be enough to cause illness. In addition to Shiga toxin, some strains of STEC contain genes that code for the ability to attach and damage intestinal tract cells, causing what is commonly referred to as attaching and effacing lesions. When a STEC has the full complement of these virulence genes and has been associated with an illness such as bloody diarrhea, it is often referred to as enterohemorrhagic *E. coli* (EHEC).

E. coli O157:H7 are easily differentiated biochemically from other enteric *E. coli* because they ferment sorbitol slowly, whereas other *E. coli* usually readily ferment sorbitol. Since the organism's first recognition as a human pathogen in 1982, diagnostic screening assays that capitalize on this difference have become widely used in clinical laboratories (Wells et al. 1983). This practice has resulted in the generation of much more information on *E. coli* O157:H7 than that available on non-O157 STEC.

The ability to detect *E. coli* O157:H7 in laboratory samples has recently been improved by the development of a separation technique that uses immunomagnetic beads. In this method, microscopic, iron cored beads are coated with antibody specific to *E. coli* O157:H7 (Okrend et al. 1992). The antibody coated beads capture *E. coli* O157:H7 organisms, and in turn, the bead-cell complexes are captured using a magnetic concentrator. These complexes can then be removed from the sample and plated onto MacConkey sorbitol agar for culture and isolation of *E. coli* O157:H7. This method has been especially useful for samples that have potentially large numbers of background organisms, such as meat products and feces, in which the growth of other bacterial species can obscure *E. coli* O157:H7 colonies during culture.

In the United States, several outbreaks have occurred from exposure to non-O157 STEC. In Montana, 18 persons developed bloody diarrhea in 1994 after exposure to contaminated milk; *E. coli* O104:H21 was cultured from the stools of three of these patients (CDC 1995). *E. coli* O111:H8 was responsible for an outbreak of gastrointestinal illness, including bloody diarrhea, in 56 persons who attended a camp in Texas in 2000 (CDC 2000a). Non-O157 serotypes of *E. coli*, including O26:H11, O111:H8, O103:H2, O113:H21, and O104:H21, have been responsible for a few outbreaks throughout the world. In a cluster of three cases of HUS caused by O113:H21 in Australia, this organism was found not to have genes coding for attaching and effacing (Paton et al. 1999).

A recent Nebraska study of stool samples from persons with a differential diagnosis of bacterial gastroenteritis found 6 (1.8%) of 335 samples positive for *E. coli* O157:H7, whereas 8 samples were positive for non-O157 STEC (Fey et al. 2000). In Washington state, a 1-year prospective study tested 445 stool samples from children who had diarrhea and isolated a non-O157 STEC from 13 (1.1%) patients and *E. coli* O157:H7 from 5 (2.9%) patients (Bokete et al. 1993). A national study of postdiarrheal HUS estimated that less than 20% of HUS cases were due to non-O157 STEC; however, the authors qualified that estimate, commenting that it was difficult to determine the proportion of STEC-associated HUS that resulted from non-O157 STEC (Banatvala et al. 2001).

Most clinical laboratories in the United States do not routinely screen for non-O157 STEC because of the lack of a biochemical marker (Mead and Griffin 1998). In addition, surveillance for cases of non-O157 STEC infection is not routinely conducted. Mead et al. (1999) estimated that the incidence of non-O157 STEC is 20% to 50% that of *E. coli* O157:H7 infection. Therefore, because *E. coli* O157:H7 is the most important STEC serotype in the United States in terms of public health and because of the current paucity of epidemiologic data for non-O157 STEC, this risk assessment is limited to *E. coli* O157:H7.

SOURCES OF *E. COLI* O157:H7

E. coli O157:H7 has been isolated from the feces or gastrointestinal tract of cattle, sheep, horses, pigs, turkeys, dogs, and a variety of wild animal species (Kudva et al. 1996; Rice and Hancock 1995; Hancock et al. 1998b; Heuvelink et al. 1999); however, epidemiologic studies have found that cattle manure is the source of most human *E. coli* O157:H7 infections. *E. coli* O157:H7 has also been isolated from bodies of water (e.g., ponds, streams), wells, and water troughs and has been found to survive for months in manure and water trough sediments (Wang and Doyle 1998; Hancock et al. 1998a; Kudva et al. 1998; Sargeant et al. 2000).

Colonization of the gastrointestinal tract for longer than 2 or 3 months has not been reported in any species, although only cattle, sheep, and humans have been sampled with sufficient intensity to assess duration of carriage (Hancock et al. 1998a). Despite this finding, *E. coli* O157:H7 has been described as "ubiquitous" in dairy and beef cattle and is present at least occasionally on most farms or feedlots (Hancock et al. 1998a; Hancock et al. 2001). This widespread prevalence in cattle has been attributed to the organism's ability to survive for at least 4 months in water trough sediments, providing an ongoing source of exposure to cattle (Hancock et al. 1998a). *E. coli* O157:H7 is also present in purchased animal feeds; therefore, such feeds may be an important route by which *E.* coli O157:H7 is disseminated to farms (Hancock et al. 2001). From the farms, *E. coli* O157:H7 contamination of meat occurs when beef carcasses come into contact with hides and feces during the slaughter process (Elder et al. 2000).

EPIDEMIOLOGY OF DISEASE DUE TO INFECTION WITH *E. COLI* O157:H7

E. coli O157:H7 was designated by the Council of State and Territorial Epidemiologists as a nationally notifiable disease in 1994. From 1994 to 2000, the number of reported cases of *E. coli* O157:H7 in the United States increased by 211%, from 1,420 (0.8 per 100,000 population) in 1994 to 4,410 (approximately 1.6 per 100,000 population) in 2000 (CDC 1999a; CDC 2001b) (Figure 2-1). Cases are reported by passive surveillance through the National Notifiable Diseases Surveillance System (NNDSS). Health care providers use this system to report notifiable disease cases to local or state health departments. The increase in reported cases over time is probably due to a combination of factors including (1) improvement in the effectiveness of the surveillance system; (2) greater awareness of *E. coli* O157:H7 infection among health care providers and the public, which has led to improved detection and reporting; (3) enhanced ability to detect disease through better diagnostic tests; and (4) a true increase in the incidence of disease.

In 1996, the Emerging Infections Program, Foodborne Diseases Active Surveillance Network (FoodNet) began a program of active surveillance of clinical laboratories for specific foodborne diseases, including *E. coli* O157:H7. Five states participated initially (Minnesota, Oregon, and selected counties of California, Connecticut, and Georgia); as of 2000, eight states were under active surveillance, representing 29.5 million persons (10.8% of the 1999 U.S. population) (CDC 2001a). The number of cases of *E. coli* O157:H7 infection reported annually to FoodNet ranged from 388 in 1996 to 631 in 2000 (Bender et al. 2000; CDC 2000c; CDC 2001a). Because the population under surveillance has increased, it is more appropriate to compare the number of reported cases per 100,000 population. For 1996 to 2000, there were 2.7, 2.3, 2.8, 2.1, and 2.9 reported cases per 100,000 population, respectively, for the five original states (CDC 2001a). Data on the prevalence of symptomatic *E. coli* O157:H7 infection prior to the inception of FoodNet are scarce. Ostroff et al. (1989) reported an incidence of 2 cases per 100,000

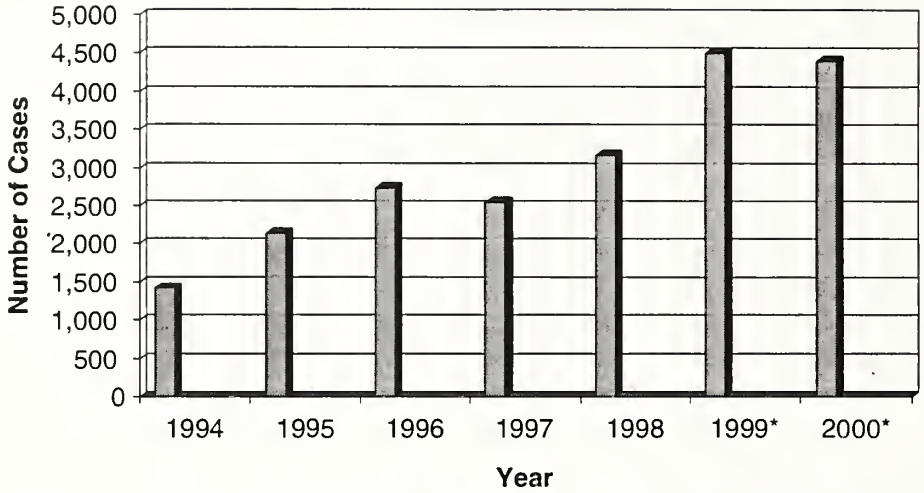

FIGURE 2-1 Number of reported cases of *E. coli* O157:H7 infection, United States, 1994–2000. *Provisional. Sources: CDC, NNDSS.

population during the first year of statewide surveillance in Washington in 1987. A prospective, population-based study, also conducted in Washington, estimated the incidence of culture-confirmed *E. coli* O157:H7 infection to be 8 per 100,000 enrollees in a Seattle-based health maintenance organization during 1985 to 1986 and 10 per 100,000 enrollees in 1987 (MacDonald et al. 1988; Ostroff et al. 1989). The results of this latter study may provide a more accurate estimate of the incidence of *E. coli* O157:H7 infection and suggest that substantial underreporting occurred in the statewide passive surveillance program.

The incidence of *E. coli* O157:H7 infection varies by age group, with the highest incidence of reported cases occurring in children. In 1998, the incidence in children younger than 1 year of age was 2.01 per 100,000 population. The highest incidence was found in 1- to 4-year-olds at 4.57 reported cases per 100,000 population, whereas 5- to 14-year-olds had an incidence of 1.83 reported cases per 100,000 population (CDC 1999a). The lowest incidence occurred in persons aged 15 or older and ranged from 1.15 to 0.61 reported cases per 100,000 population. At FoodNet sites in 1999, 35.3% of reported cases occurred in 1- to 10-year-olds, 17.6% of cases occurred in 10- to 20-year-olds, and 14.1% of cases occurred in persons older than 60 (CDC 2000b). Other studies have also found a high incidence in children (Ostroff et al. 1989; Proctor and Davis 2000).

Diagnosis of *E. coli* O157:H7 is more common in the summer months (Mead and Griffin 1998). Of cases reported by FoodNet sites, 70% occurred during June through September for the years 1996 to 1998 (Bender et al. 2000). In 1998, 1,710 (54.1%) of 3,161 cases of *E. coli* O157:H7 reported through NNDSS to CDC occurred during those months (CDC 1999a). Outbreaks also occur more frequently in the summer, with 50 (58.8%) of 85 foodborne outbreaks occurring during June through September for the period 1993 to 1997 (CDC 1999a). During 1998 to 1999, 21 (50.0%) of 42 foodborne outbreaks occurred during June through September (CDC 2000c; CDC 2001c).

Most postdiarrheal HUS cases are thought to be due to *E.* coli O157:H7 infection. In a study of 83 patients infected with HUS between 1987 and 1991, STEC was implicated as the cause of illness in 72% of the patients; more than 80% of these cases were caused by *E. coli* O157:H7 infection (Banatvala et al. 2001). Siegler et al. (1994) found that 140 (89.2%) of 157 HUS cases that occurred in Utah between 1971 and 1990 were postdiarrheal. *E. coli* O157:H7 testing was only available for the last 4 years of this study, but the authors concluded that *E. coli* O157:H7

may have been the leading cause of HUS in that region of the United States for the duration of the study period (Siegler et al. 1994).

HUS has been a nationally notifiable disease since 1996, and cases are reported by passive surveillance through NNDSS. Active surveillance for HUS in children at FoodNet sites began in 1997. In 1998, the most recent year for which data are available, 90 cases of HUS were reported through NNDSS (CDC 1999a). In 1999, 60 cases were reported and 8 (13.3%) deaths occurred at FoodNet sites (CDC 2000b). HUS occurs more commonly in children than adults. During 1997 to 1999 at FoodNet sites, the overall incidence of HUS among children younger than 15 years of age was 0.7 per 100,000 population; for children younger than 5, the incidence was 1.4 per 100,000 (CDC 2000b). In a nationwide study of 83 patients with HUS, 46 (55.4%) were younger than 5 years old and an additional 27 (32.5%) were 5 to 17 years old (Banatvala et al. 2001).

Similar to the seasonal distribution in reported cases of *E. coli* O157:H7 infection, HUS cases occur more frequently in summer months. In 1998 and 1999, respectively, 31 (59.6%) of 52 reported HUS cases and 41 (68.3%) of 60 cases in the United States occurred during June through September (CDC 1999a; CDC 2000b). Additional details about HUS can be found in the section below on adverse health outcomes associated with *E. coli* O157:H7 infection.

The number of reported *E. coli* O157:H7 cases derived from surveillance is known to be an underestimate of the true disease burden. Underestimation of the actual incidence of infection occurs for a variety of reasons:

- Some infected persons do not seek medical care.
- Physicians do not perform diagnostic testing on all patients who have symptoms of infection.
- Some persons who obtain medical care do not provide a stool specimen.
- Laboratories do not culture all stool samples for *E. coli* O157:H7.
- Some proportion of laboratory results are false negatives.
- Not all culture-confirmed infections are reported to public health authorities by health care providers and laboratories.

For example, in a 1994 national survey, 70 (54.3%) of 129 randomly selected clinical laboratories reported that they did not routinely test all stools or all bloody stools for *E. coli* O157:H7 (Boyce et al. 1995b). However, routine culturing of bloody diarrhea for *E. coli* O157:H7 is increasingly common, particularly in FoodNet sentinel site areas. Using surveillance data and accounting for the factors that contribute to underreporting, Mead et al. (1999) estimated that 73,480 cases of *E. coli* O157:H7 infection occur annually in the United States and that 85% (62,456 cases) are a result of foodborne exposure.

TRANSMISSION OF *E. COLI* O157:H7

To choose the most appropriate product to model in this risk assessment, we assessed how frequently various products were implicated in *E. coli* O157:H7 infection by evaluating studies of sporadic cases of *E. coli* O157:H7 infection and outbreak investigation reports. Sporadic cases account for the majority of reported cases in a given year and therefore may be more representative of persons with *E. coli* O157:H7 infection. For example, 75% of reported cases in Oregon during 1991 to 1997 and 83% of reported cases in Wisconsin during 1992 to 1999 were sporadic (OCD 1998; Proctor and Davis 2000).

In the first nationwide case-control study of sporadic *E. coli* O157:H7 infection, conducted in 1990 to 1992, consumption of undercooked ground beef (described as "pink in the middle") was the only dietary factor independently associated with diarrhea in multivariate analysis. The

population-attributable risk for this behavior was 34% (Slutsker et al. 1998). A study of sporadic cases of *E. coli* O157:H7 infection in New Jersey found that these individuals were more likely than healthy controls to have eaten a hamburger in the week preceding illness (Mead et al. 1997). In addition, patients were slightly more likely than controls to report having eaten a hamburger that was pink in the middle (45% vs. 33%) (Mead et al. 1997). Kassenborg et al. (2001) also found that consumption of pink hamburgers or pink ground beef was a statistically significant risk factor, although merely consuming ground beef was not. Other significant risk factors by multivariate analysis were exposure to farms or to cattle, eating at a table service restaurant, using immune suppressive medication (for adults only), and obtaining beef through a private slaughter arrangement. This study estimated the population-attributable risk from consuming pink hamburger was 8% for meals consumed at home and 7% for meals consumed away from home and was 18% for farm exposures (visiting or living on a farm) (Kassenborg et al. 2001).

A prospective study in Washington state identified that rare ground beef was consumed more often by cases than controls (MacDonald et al. 1988). A Canadian study of sporadic cases conducted in 1990 identified consumption of undercooked ground beef as a risk factor for *E. coli* O157:H7 infection; the attributable risk was 17% (Le Saux et al. 1993). In a case-control study of sporadic cases conducted in Oregon during 1996 to 1997, visiting or living on a farm where cattle were present was a risk factor associated with *E. coli* O157:H7 infection (OCD 1998).

Outbreak investigations have contributed significantly to our understanding of how *E. coli* O157:H7 is transmitted. Since the first recognized ground beef-associated outbreak in 1982 (Riley et al. 1983), outbreaks have been attributed to foodborne, waterborne, and person-to-person means of transmission. In 13 outbreaks that occurred between 1982 and 1993 in the United States, the transmission source was identified as hamburger or ground beef in 7 (53.9%) (Griffin 1995).

A total of 128 foodborne outbreaks due to *E. coli* O157:H7 infection were reported in the United States between 1993 and 1999; of these, the food vehicle was identified in 92 (71.9%) (CDC 1999b; CDC 2000c; CDC 2001c). These 92 outbreaks involved 4,421 cases, with a range of 324 to 1,340 cases per year attributable to outbreaks. Beef was the food item most frequently associated with outbreaks. Of the 92 outbreaks with an identified food vehicle, 42 (45.7%) were attributed to exposure to beef. The specific beef product was not identified for 1993 to 1997 outbreaks, but for the 21 beef-associated outbreaks that occurred during 1998 to 1999, ground beef or hamburger was identified as the vehicle in 19. Two outbreaks in 1999 were attributed to roast beef, and one of these was a result of environmental contamination from manure in a pasture where a picnic was held. A list of food vehicles implicated during 1998 to 1999 outbreaks is shown in Table 2-1. Of the 19 ground beef/hamburger-associated outbreaks, 5 (26.3%) occurred in multiple states.

In summary, individuals can be exposed to *E. coli* O157:H7 in many ways. Current data based both on outbreaks and on sporadic infections indicate that consumption of ground beef is the primary source of *E. coli* O157:H7 exposure. For these reasons, ground beef is the focus of this *E. coli* O157:H7 risk assessment.

ADVERSE HEALTH OUTCOMES ASSOCIATED WITH *E. COLI* O157:H7

Ingestion of *E. coli* O157:H7 results in a wide range of possible outcomes, from asymptomatic infection to death. To cause disease, the *E. coli* O157:H7 must survive acidic conditions within the stomach before moving to distal portions of the gastrointestinal tract. Disease due to *E. coli*

TABLE 2-1 Food Vehicles Implicated in Outbreaks of *E. coli* O157:H7, United States, 1998–1999

Vehicle	1998	1999	Total
Ground beef/hamburger	10	9	19
Roast beef	0	2	2
Lettuce	1	3	4
Coleslaw	2	1	3
Salad	1	1	2
Milk	2	0	2
Tacos	0	1	1
Apple cider	0	1	1
Game meat	0	1	1
Cake	1	0	1
Cheese curd	1	0	1
Fruit salad	1	0	1
Macaroni salad	1	0	1
Multiple	1	0	1
Unknown	0	2	2
Total	21	21	42

Sources: CDC 1999b; CDC 2001c.

O157:H7 occurs primarily in the colon. The incubation period from the time of ingestion to the first symptoms ranges from 1 to 8 days. Asymptomatic shedding of *E. coli* O157:H7 has been documented (Swerdlow and Griffin 1997); however, the proportion of exposed individuals who shed *E. coli* O157:H7 but do not develop symptoms is unknown. Typically the illness begins with abdominal cramps and nonbloody diarrhea, which can, but does not necessarily, progress to bloody diarrhea within 2 to 3 days (Griffin 1995; Mead and Griffin 1998). More severe manifestations of *E. coli* O157:H7 infection include hemorrhagic colitis (grossly bloody diarrhea), HUS (a combination of renal failure, low platelet counts, and hemolytic anemia), and occasionally TTP. Approximately 30% to 45% of patients are hospitalized (Ostroff et al. 1989; Le Saux et al. 1993; Bell et al. 1994; Slutsker et al. 1998). Of the 631 cases reported to FoodNet sites in 1999, 39% were hospitalized (CDC 2000c). Treatment for the more serious manifestations of *E. coli* O157:H7 infection is supportive, and the use of antimicrobial agents has been debated (Mead and Griffin 1998).

Of symptomatic patients, 70% or more usually develop bloody diarrhea (Mead and Griffin 1998). A total of 451 (90.0%) of 501 cases, most of whom were stool culture positive for *E. coli* O157:H7, developed bloody diarrhea during a large outbreak in four western states in 1993 (Bell et al. 1994). In a study of sporadic cases in Washington state, 84 (95.5%) of 88 cases developed bloody diarrhea (Ostroff et al. 1989). However, patients with bloody diarrhea are more likely to seek medical attention, so these estimates may be subject to ascertainment bias. Symptoms of hemorrhagic colitis include severe abdominal cramps followed by grossly bloody diarrhea and edema (swelling), erosion, or hemorrhage of the mucosal lining of the colon (Su and Brandt 1995). Hemorrhagic colitis may be the only manifestation of *E. coli* O157:H7 infection, or it may precede development of HUS. Complications from hemorrhagic colitis associated with *E. coli* O157:H7 include upper-gastrointestinal bleeding and stroke (Su and Brandt 1995). Roberts et al. (1998, citing Boyce et al. 1995a; Ryan et al. 1986) estimate the mortality rate of those suffering hemorrhagic colitis without progression to HUS to be 1%, although Griffin (personal communication) believes that this rate is too high.

The proportion of all patients who develop HUS following *E. coli* O157:H7 infection varies among sporadic cases and outbreak-associated cases. Between 3% and 7% of sporadic cases and 20% or more of outbreak-associated cases of *E. coli* O157:H7 infection will progress to HUS (Mead and Griffin 1998). The proportion of patients who develop HUS following *E. coli* O157:H7 infection is influenced by a variety of factors, including age, bloody diarrhea, fever, elevated leukocyte count, and toxin type (Griffin 1995). Wong et al. (2000) found that 10 (14.1%) of 71 children with *E. coli* O157:H7 infection developed HUS.

HUS is the most common cause of acute renal failure in young children, yet it also has long-term complications. Siegler et al. (1994) found that HUS causes chronic renal sequelae, usually mild, in 51% of survivors (48% of all cases). Neurologic complications occur in about 25% of HUS patients (Mead and Griffin 1998). Neurologic symptoms are generally mild, but serious complications, such as seizure, stroke, and coma, can occur (Su and Brandt 1995). Similar to treatment for *E. coli* O157:H7 infection, only symptomatic treatment is available for neurologic complications, making this manifestation of HUS especially dangerous and an important cause of death in HUS patients. Other complications of HUS include pancreatitis, diabetes mellitus, and pleural and pericardial effusions (Mead and Griffin 1998). In a nationwide study of HUS patients, 46 (55%) of 83 patients required either peritoneal dialysis or hemodialysis during the acute phase of their illness (Banatvala et al. 2001). Siegler et al. (1994) found that severe kidney or neurological impairments (end stage renal disease or stroke) occurred in 9 (5.7%) of 157 HUS cases over a 20-year period in Utah. Using 1990 Medicare data on survival rates after kidney transplantation and survival rates on dialysis for pediatric patients, Buzby et al. (1996) estimated that approximately 60% of pediatric HUS patients who develop chronic kidney failure die prematurely.

On the basis of long-term studies in Minnesota (Martin et al. 1990) and King County, Washington (Tarr and Hickman 1987), and a 2-year, nationwide study in Canada, Rowe et al. (1991) and Mahon et al. (1997) estimated the acute mortality rate for HUS at 3% to 5%. In the study by Banatvala et al. (2001), 4 (6.5%) of 62 children with HUS died, and neither of 2 adults with HUS died. A long-term study in Utah reported 5% mortality (Siegler et al. 1994).

Occasionally, patients with *E. coli* O157:H7 are diagnosed as having TTP, a condition similar to HUS but more likely to occur in adults and with more prominent neurological findings and less renal involvement. Of 73 children and 10 adults who met the case definition for HUS in the study by Banatvala et al. (2001), 8 (11.0%) children and 8 (80.0%) adults also met the case definition for TTP. None of the children died, but 2 (25.0%) of the adults did. There are many causes of TTP other than the association with *E. coli* O157:H7, and prior to the 1980s, gastrointestinal infections had not been strongly implicated in the pathogenesis of TTP (CDC 1986). When associated with *E. coli* O157:H7 infection, TTP is probably the same disorder as HUS (Mead and Griffin 1998).

PATHOGENESIS

It is not our goal to provide a detailed review of Shiga toxin-producing *E. coli* pathogenesis, and interested readers are referred to recent publications (Paton and Paton 1998; Nataro and Kaper 1998). By definition, all STEC produce Shiga toxins; although it appears that the production of Shiga toxins is a critical factor in the pathogenesis of *E. coli* O157:H7-related disease, other important virulence factors exist as well (see below). There are two main types of Shiga toxin: Shiga toxin 1 and Shiga toxin 2. STEC strains may produce either Shiga toxin 1 or Shiga toxin 2 or both, and the genes for the toxins are encoded on lysogenic bacteriophages within the STEC chromosome. Shiga toxin 1 is almost identical to the Shiga toxin produced by *Shigella*

dysenteriae type 1, and Shiga toxin 2 is approximately 55% homologous. A second important set of virulence factors in many STEC strains is a series of genes in a 35-kilobase pathogenicity island known as the Locus for Enterocyte Effacement (LEE) (Nataro and Kaper 1998; Paton and Paton 1998). A similar pathogenicity island was first described in enteropathogenic *E. coli* (EPEC). Many of the genes within the LEE are involved in the interaction of the bacteria with the human intestinal epithelial cell barrier. For example, the *eae* gene encoded on LEE encodes a protein expressed on the bacterial surface that is critical for the close attachment of the bacteria to the host cell. Other LEE genes are involved in this bacterial docking process and in changes that occur in the host cell following bacterial interaction. Virtually all *E. coli* O157:H7 strains possess the LEE. However, some STEC strains known to be associated with HUS, such as an O113:H21 strain described in Australia (Paton et al. 1999), lack the LEE but are clearly still pathogenic. Most *E. coli* O157:H7 strains also have a 60 mega dalton plasmid that encodes enterohemolysin (hlyA), among other things. The role of the plasmid in virulence is unknown.

FACTORS AFFECTING SURVIVAL AND GROWTH OF *E. COLI* O157:H7 IN FOOD

A number of factors have a significant influence on the survival and growth of *E. coli* O157:H7 in food, including temperature, pH, salt, and water activity (Meng and Doyle 1998). Studies on the thermal sensitivity of *E. coli* O157:H7 in ground beef have revealed that the pathogen has no unusual resistance to heat and that heating ground beef sufficiently to kill typical strains of *Salmonella* will also kill *E. coli* O157:H7. Thermal pasteurization of milk has also been determined to be an effective treatment (Doyle et al. 1997). The optimal temperature for growth of *E. coli* O157:H7 is approximately 37°C (98.6°F), and the organism will not grow at temperatures below 8°C to 10°C (46°F to 50°F) or above 44°C to 45°C (Doyle and Schoeni 1984; Buchanan and Doyle 1997). *E. coli* O157:H7 survives freezing, with some decline in the concentration of *E. coli* O157:H7 (Ansay et al. 1999).

E. coli O157:H7 has been reported to be more acid resistant than other *E. coli*. Acid resistance enhances the survival of *E. coli* O157:H7 in mildly acidic foods and may explain its ability to survive passage through the stomach and cause infection at low doses. The ability to be acid resistant varies among strains and is influenced by growth phase and other environmental factors. Once induced, acid resistance is maintained for long periods of time during cold storage (Meng and Doyle 1998). Stationary-phase *E. coli* O157:H7 are more resistant than growing cells to acid (Meng and Doyle 1998). The presence of other environmental stresses, such as temperature or water activity stress, will raise the minimum pH for growth (Buchanan and Doyle 1997). *E. coli* O157:H7 survives in such foods as dry salami, apple cider, and mayonnaise, which were previously considered too acidic to support the survival of foodborne pathogens. Published literature contains conflicting reports about the efficacy of acid spray washing of beef carcasses. A study by Brachett et al. (1994) found that warm and hot acid sprays did not significantly reduce the concentration of *E. coli* O157:H7 on beef carcasses. Two recent studies have found organic acids to be effective in reducing the presence of *E. coli* O157:H7 on beef carcasses (Berry and Cutter 2000; Castillo et al. 2001). These apparently contradictory results may reflect differences in acid resistance among strains of *E. coli* O157:H7 (Berry and Cutter 2000).

E. coli O157:H7 can survive for extended periods under conditions of reduced water activity while refrigerated; however, the organism does not tolerate high salt conditions (Buchanan and Doyle 1997).

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3

Exposure Assessment

This chapter describes the model used to estimate the occurrence of *Escherichia coli* O157:H7 in single servings of ground beef. This exposure model is divided into three modules: production, slaughter, and preparation. The production module estimates the occurrence of *E. coli* O157:H7 infection in two populations of live cattle: culled breeding cattle (cows and bulls) and cattle fed specifically for slaughter (steers and heifers). The slaughter module estimates the occurrence and extent of *E. coli* O157:H7 on carcasses and in beef trim combined in 2,000-pound combo bins or 60-pound boxes. The preparation module estimates the occurrence of *E. coli* O157:H7 in single servings of cooked ground beef. When appropriate, the effects of storage (e.g., chilling) and cooking are included throughout the model to account for organism growth or decline with resultant increased or decreased numbers of *E. coli* O157:H7. Exposure to *E. coli* O157:H7-contaminated ground beef servings was analyzed by age of the consumer and location where the meal was consumed (i.e., home or away from home). Each module of the exposure assessment model—production, slaughter, and preparation—yields one or more output distributions that serve either as inputs to the next module or as summary outputs.

PRODUCTION MODULE

The production module estimates the prevalence of *E. coli* O157:H7-infected cattle entering U.S. slaughter plants. It models culled breeding cattle (cows and bulls) and feedlot cattle (steers and heifers) at their points of origin through transit to the slaughter plant.

We know that *E. coli* O157:H7-infected cattle entering the slaughter process may influence the contamination of ground beef. A determination of the quantitative association between the incoming status of cattle and the outgoing status of harvested meat is critical in this exposure assessment. This quantitative correlation between pre-harvest and post-harvest contamination is best predicted using fecal *E. coli* O157:H7 prevalence data (Elder et al. 2000).

Explanation of Scope

The *E. coli* O157:H7 exposure assessment starts where beef production begins—at the farm. Most evidence on the occurrence and distribution of this organism in U.S. livestock was collected during surveys of farms and feedlots. Therefore, estimating the proportion of *E. coli* O157:H7-infected cattle at slaughter begins with estimating the proportion of infected cattle on the farm.

Imported beef is assumed to originate from countries whose *E. coli* O157:H7 epidemiology is similar to the United States. Approximately 15% of the fresh, chilled, and frozen beef and veal consumed in the United States is imported, and 90% of imports originate in Australia, New Zealand, and Canada (APHIS:VS:CEAH 1994). Specific data regarding the prevalence of *E. coli* O157:H7 in beef imported from various countries are lacking, and published surveillance data from the three major exporters to the U.S. are variable. However, evidence indicates that *E. coli* O157:H7 occurs in Australian, New Zealand, and Canadian cattle and humans (Robins–Browne et al. 1998; New Zealand Public Health Report 2000; Spika et al. 1998). In general, this evidence does not suggest that the prevalence of *E. coli* O157:H7 is dramatically greater in those countries than in the United States. Because this analysis intends to model all ground beef consumed in the United States, we assume that the share of imported ground beef that is contaminated is similar to the share of domestic ground beef that is contaminated.

The prevalence of infected cattle entering slaughter plants may be reduced through actions on the farm or feedlot. Many risk factors thought to influence *E. coli* O157:H7 status in cattle apply to whole herds rather than to individual cattle. For example, certain feed or feeding practices are hypothesized to elevate the probability of cattle becoming colonized with *E. coli* O157:H7 (Dargatz et al. 1997; Hancock et al. 1997b, 1998a; Herriot et al. 1998; Cray et al. 1998; Diez–Gonzales et al. 1998). Therefore, mitigation strategies typically target herd-level risk factors for *E. coli* O157:H7 control. For example, vaccination for *E. coli* O157:H7 would likely be applied at the herd level (Jordan et al. 1999; Gyles 1998).

Culled breeding cattle and feedlot cattle are separately modeled in this risk assessment. The slaughter, processing, and distribution of meat from these types of cattle are different. Furthermore, sampling evidence suggests that there may be differences in *E. coli* O157:H7 prevalence between these two types of cattle.

Breeding cattle comprise animals from dairy and beef cow-calf herds. In both types of breeding herds, mature cattle are bred to produce milk and calves. About 20% of all cattle slaughtered in the United States are breeding cattle (FSIS 1998). Feedlot cattle are steers and heifers sent to slaughter from feedlots. About 80% of all cattle slaughtered in the United States are feedlot cattle (FSIS 1998).

Definition of Key Terms

The following key terms are used throughout this module:

- Prevalence is the proportion of infected herds or individual cattle in a population.
- Herd prevalence is the proportion of herds with one or more *E. coli* O157:H7-infected cattle when the reference population is all herds of one type—for example, breeding herds.
- Apparent herd prevalence is the proportion of herds with one or more test-positive cattle detected among all herds sampled. Positive cattle are those animals that were diagnosed as infected or contaminated, based on testing. It is assumed that when microbiologic culture is used, all test-positive cattle are truly infected. "Infected" refers to cattle whose

intestinal tracts are colonized with the *E. coli* O157:H7 organism. "Contaminated" refers to cattle whose hides, hair, or hooves have some *E. coli* O157:H7 organisms residing on them. At present, no studies have specifically addressed the occurrence of contaminated cattle in herds, so the prevalence of infected herds is estimated based exclusively on infected cattle evidence. Given the limited understanding of the ecology of *E. coli* O157:H7 in cattle herds, it is assumed that contaminated cattle can only reside within herds that have one or more infected cattle.

- True herd prevalence is estimated by adjusting apparent herd prevalence observed in surveys with herd sensitivity.
- Herd sensitivity is the proportion of infected herds that, when tested, are detected as *E. coli* O157:H7-positive. Herd sensitivity is dependent on the number of samples collected within herds and the detectable prevalence of infected animals in the infected herds.
- Within-herd prevalence is the proportion of infected cattle when the reference population is the cattle within a specific infected herd. By convention, within-herd prevalence estimates only apply to infected herds. By definition, noninfected herds have a within-herd prevalence of 0%.
- Apparent within-herd prevalence is the proportion of *E. coli* O157:H7-positive cattle detected in a sample of cattle from an infected herd.
- True within-herd prevalence is estimated by adjusting the apparent within-herd prevalence observed in surveys by test sensitivity.
- Test sensitivity is the proportion of infected cattle that, when tested, are detected as *E. coli* O157:H7-positive using a particular diagnostic test. Test sensitivity is a complex parameter that incorporates variability in sample collection and handling and in the biological properties of the sample.

Production Module Segments

The production module comprises three segments: on-farm, transportation, and slaughter plant intake. As noted previously, culled breeding cattle ("breeding herds") are considered separately (Figure 3-1A) from feedlot cattle ("feedlots") (Figure 3-1B). The on-farm segment estimates the prevalence of *E. coli* O157:H7-infected herds (herd prevalence) and of *E. coli* O157:H7-infected cattle in infected herds (within-herd prevalence). Variability of within-herd prevalence among all infected herds—and by season of the year—is also estimated. The transportation segment considers the effect of transit time and commingling on the transmission and amplification of *E. coli* O157:H7 infections. The slaughter plant intake segment considers the effect of clustering cattle as they enter the slaughter plant. The following sections describe data and analysis for each of these segments.

On-Farm Segment

Breeding Herd Prevalence

Herd prevalence is the proportion of all breeding herds that contain one or more infected cattle. It is assumed that herd prevalence remains constant over time at a national level.

Hypothetically, herd prevalence might change across seasons or years. Seasonal changes in herd prevalence have been suggested (Garber et al. 1999), but these changes are most reasonably explained as the result of seasonal changes in the within-herd prevalence for infected herds. Seasonal variation in within-herd prevalence has been previously reported (Hancock et al. 1994,

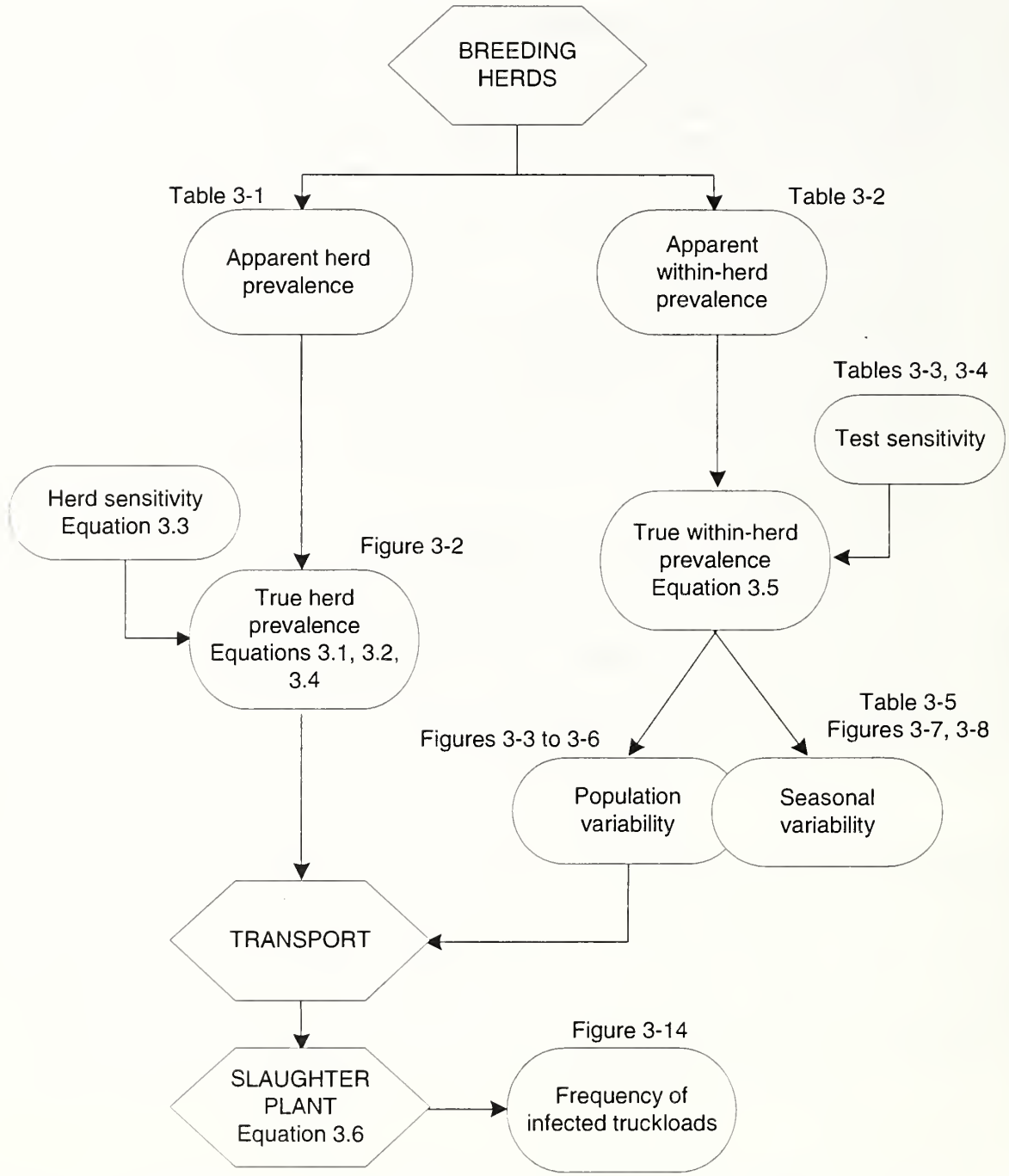

FIGURE 3-1A Production module flowchart for estimation of key variables for breeding herds (cows and bulls).

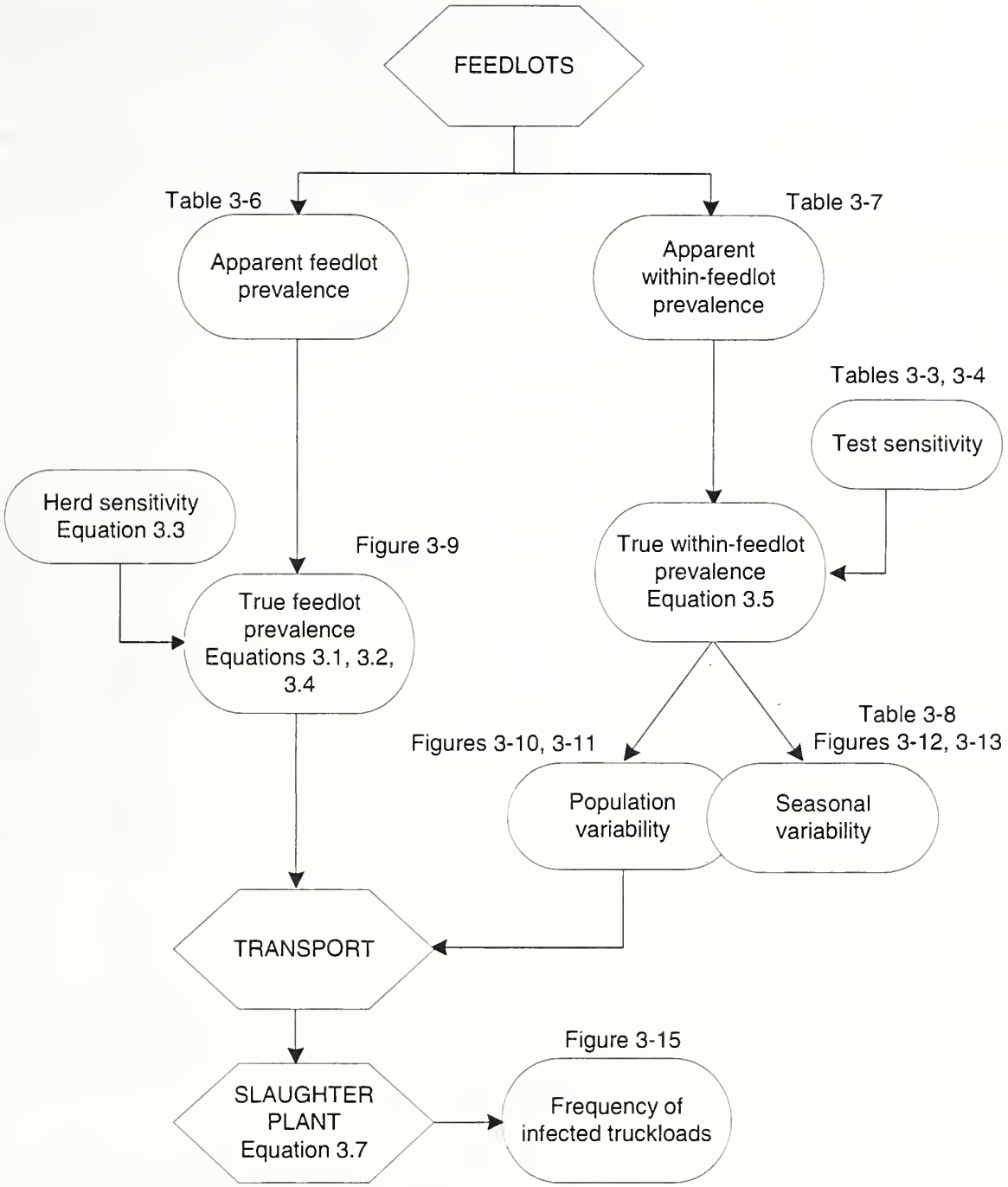

FIGURE 3-1B Production module flowchart for estimation of key variables for feedlot herds (steers and heifers).

1997b; Heuvelink et al. 1998). If within-herd prevalence varies by season, then the apparent herd prevalence detected in surveys will also vary in a similar pattern (assuming sample size within herds is constant). While herd prevalence might change across years, there is no empirical evidence supporting such a change in the past 5 years.

Herd prevalence is estimated using evidence that may have been generated from sampling herd subpopulations other than mature cattle. Yet evidence about the existence of *E. coli* O157:H7 within any age of cattle in a herd indicates that cows or bulls culled from that herd might be infected.

Apparent Breeding Herd Prevalence

Seven studies provide evidence regarding the apparent prevalence of infected breeding herds (Table 3-1). Nearly all studies sampled herds from multiple states in the United States.

TABLE 3-1 Evidence Used to Estimate Breeding Herd Prevalence

Study	Herds Tested	Positive Herds	Apparent Herd Prevalence	Average Samples Per Herd	Apparent Within-Herd Prevalence	Lab Methods	Months Sampled
Hancock et al. 1997a	13	9	69%	791	1.3%	0.1 g, SMACct	June–May
Hancock et al. 1997b	36	27	75%	360	1.8%	0.1 g, SMACct	July–December
Hancock et al. 1998a	6	6	100%	183	2.3%	0.1 g, SMACct	July–November
Garber et al. 1999	91	22	24%	58	4.0%	1 g, SMACct, TSB	February–July
Lagreid et al. 1999	15	13	87%	60	8.0%	10 g, IMS	October–November
Sargeant et al. 2000	10	10	100%	235	1.2%	10 g, IMS	January–December
Hancock 2001	20	18	90%	317	0.7%	0.1 g, SMACct	December–March, June–September

Note: g = grams of feces analyzed,
SMACct = sorbitol MacConkey media with cefixime and tellurite,
TSB = trypticase soy broth, and
IMS = immunomagnetic separation.

National studies have not shown any geographic clustering of *E. coli* O157:H7 among breeding herds (Garber et al. 1995, 1999). Therefore, U.S. herd prevalence data are pooled without regard for the region where the data were collected.

Hancock et al. (1997a) sampled 13 dairy herds in three northwestern states monthly for 1 year (1993 to 1994); 9 (69%) herds tested positive. Approximately 60 samples were collected on each visit from a combination of weaned heifers and adult cows. Apparent within-herd prevalence in the nine positive herds was 1%.

Hancock et al. (1997b) sampled 36 dairy herds in three northwestern states from July to December 1994; 27 (75%) of the 36 tested herds were positive. In each herd, 60 fecal samples

from post-weaned heifers were collected once a month, and about 2% of cattle within infected herds were positive.

Hancock et al. (1998a) also sampled six dairy herds in three northwestern states from July to November 1996. In each herd, 60 fecal samples from post-weaned heifers were collected once a month for 3 months. All herds tested positive. Apparent within-herd prevalence was 2.3%.

Garber et al. (1999) report on a national survey of the U.S. dairy industry conducted by the U.S. Department of Agriculture (USDA) from February to July 1996. Fecal samples were collected from 91 dairy herds across the United States, and 22 herds were found to have one or more test-positive cattle. Within each herd, the average number of samples collected was 58, and about 4% of sampled cattle in the positive herds were found to be *E. coli* O157:H7-positive.

Lagreid et al. (1999) sampled 15 cow-calf herds across five midwestern states in October and November 1997; 13 (87%) herds tested positive. In each herd, 60 fecal samples from weaned calves were collected. This study used more sensitive lab methods than many studies that preceded it. Therefore, the apparent within-herd prevalence (8%) found in this study reflects the improved capacity of that test to detect positive cattle.

Sargeant et al. (2000) sampled 10 Kansas cow-calf herds once a month for 1 year (1996 to 1997), and all 10 herds tested positive. On each visit, about 10% of the cow and bull herd was sampled (~20 head per month). This study also used very sensitive test methods but found an apparent within-herd prevalence (~1%) more consistent with studies using less sensitive methods.

Hancock (2001) is completing a study of 30 dairy herds in two northwestern states. Twenty of these herds have been sampled during the winter (December through March) and summer (June through September). Eighteen of these herds were found to contain at least one positive cattle. Apparent within-herd prevalence for adult cattle is 0.7% using moderately sensitive test methods.

True Breeding Herd Prevalence

True herd prevalence is estimated from apparent herd prevalence using Bayes Theorem:

$$f(\Phi \mid y) = \frac{f(y \mid \Phi)\, f(\Phi)}{\int_0^1 f(y \mid \Phi)\, f(\Phi)\, d\Phi} \tag{3.1}$$

Equation 3.1 predicts the distribution for true herd prevalence (Φ), given apparent prevalence evidence (y). The function, $f(y \mid \Phi)$, is the likelihood of observing a particular sampling result (e.g., 27 positive herds in 36 sampled herds from Hancock et al. 1997b), given true herd prevalence Φ. This likelihood function depends on the herd sensitivity (HSens), the number of herds sampled in a study (N), and the number found positive (S):

$$f(y \mid \Phi) = \binom{N}{S} (\text{HSens} \times \Phi)^S \, (1 - \text{HSens} \times \Phi)^{N-S} \tag{3.2}$$

The herd sensitivity (HSens) of a particular survey was defined as

$$\text{HSens} = 1 - \int (1 - p_i)^n \, f(p_i)\, dp, \tag{3.3}$$

where p_i is the apparent within-herd prevalence in herd i, $f(p_i)$ is the frequency of p_i, and n is the number of samples collected in each herd.

Using Monte Carlo methods, HSens was estimated to be 0.75 for Garber et al. (1999), 0.86 for Lagreid et al. (1999) and Sargeant et al. (2000), 0.89 for Hancock et al. (1998a) and Hancock (2001), 0.96 for Hancock et al. (1997b), and 0.99 for Hancock et al. (1997a). Apparent within-herd prevalence was assumed to be an exponential distribution (as discussed in the "Within-Breeding Herd Prevalence" section). Average within-herd prevalence was modeled using a beta(s+1,n–s+1) distribution, where s was the number of test-positive cattle in detected herds and n was the total cattle tested in detected herds (Vose 1996).

True breeding herd prevalence (Figure 3-2) was estimated by combining the results from Equation 3.2 across all seven studies using Equation 3.4:

$$f(\theta \mid x_i) = \frac{f(x_i \mid \theta)\, f(\theta_{i-1})}{\int_0^1 f(x_i \mid \theta)\, f(\theta_{i-1})\, d\theta} \tag{3.4}$$

where x_i reflects the evidence provided by study i, and $f(\theta_{i-1})$ is the prior distribution for breeding herd prevalence based on evidence provided by study $i–1$.

Figure 3-2 suggests that breeding herd prevalence is most likely 65%, but it could be as low as 50% or as high as 80% based on the available evidence. Therefore, the majority of breeding herds in the United States are predicted to contain one or more *E. coli* O157:H7-infected cattle.

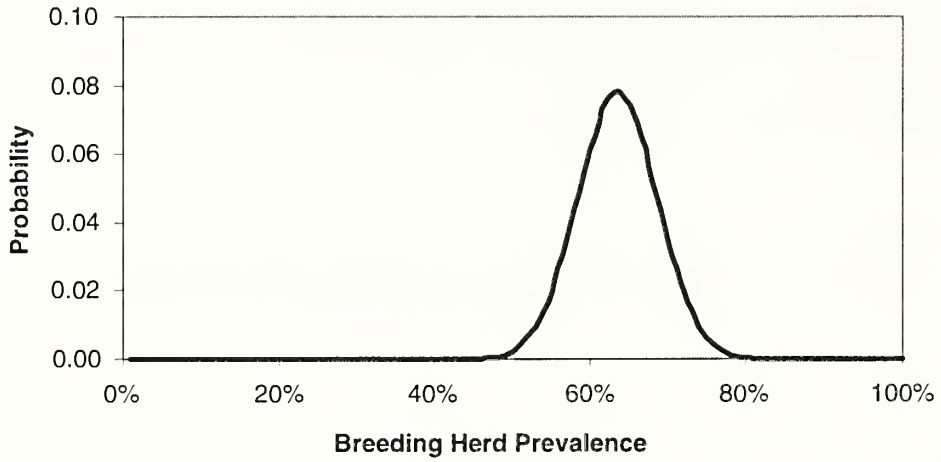

FIGURE 3-2 Resultant uncertainty distribution for true breeding herd prevalence after analysis of data in Table 3-1.

As defined in this risk assessment, breeding herds comprise dairy and cow-calf herds. Although most evidence on breeding herds was collected in dairy herds, two studies exclusively sampled cattle in cow-calf herds (Lagreid et al. 1999; Sargeant et al. 2000). Dairy cows are usually managed intensively. They are gathered at least twice daily and often confined to lots or pastures where contact between individuals is likely to occur. Commercial dairies are also very busy operations: milk trucks, feed delivery vehicles, and other visitors are common. Cows in cow-calf herds are less intensively managed. These cows usually live on large pastures throughout the year. Hypothetically, the potential for fecal-oral spread of *E. coli* O157:H7 is greater for dairy herds than for beef herds based on these management differences. Furthermore, the potential for introduction of *E. coli* O157:H7 into a dairy would seemingly be greater given the increased traffic and congestion in such operations. Yet the studies show that cow-calf herds

are no less likely to be infected than dairy herds (i.e., Lagreid et al. [1999] found 87%—and Sargeant et al. [2000] found 100%—of cow-calf herds they studied positive). Although the evidence is limited, it suggests that dairy and cow-calf herds are similar with respect to *E. coli* O157:H7.

Within-Breeding Herd Prevalence

Within-herd prevalence is the proportion of infected cattle that an infected herd might send to slaughter. Culled breeding cattle sent to slaughter are a subset of these herds. Within-herd prevalence in this model applies to just these cattle.

Apparent Within-Breeding Herd Prevalence

Within-herd prevalence varies among the population of all infected herds. If all the infected herds could be examined at a given point in time, differences in within-herd prevalence among these herds could be observed. Within-herd prevalence also varies systematically among infected herds by season (Hancock et al. 2001). Therefore, within-herd prevalence is modeled as a frequency distribution to reflect population variability, but the frequency distribution is adjusted to reflect seasonal patterns.

Population variability. Two studies provide evidence about the population variability of within-herd prevalence among known-infected herds (Hancock et al. 1997b; Garber et al. 1999). Both studies included sufficient herds (i.e., 27 and 22 herds) and samples to estimate a distribution.

Figure 3-3 is a histogram of within-herd prevalence from a study that sampled dairy heifers in three northwestern states between July and December 1994 (Hancock et al. 1997b). This histogram suggests a declining frequency of herds as within-herd prevalence increases. Its mean and standard deviation are 1.9% and 1.3%, respectively. Hypothetically, such a histogram might be generated from an exponential distribution.

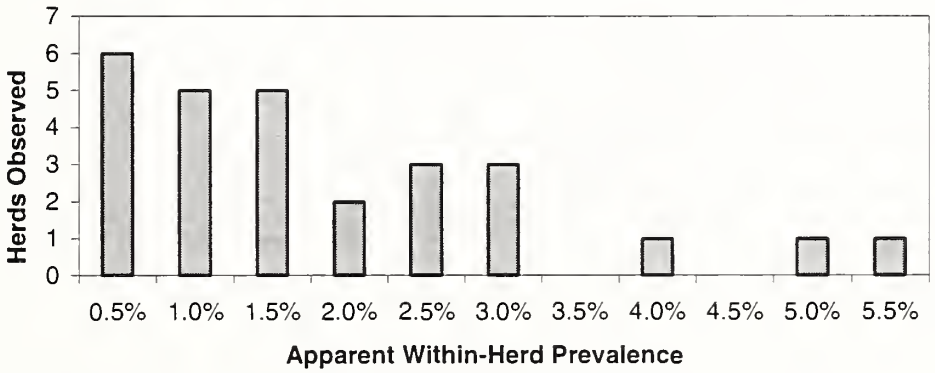

FIGURE 3-3 Evidence on the distribution of within-herd prevalence of *E. coli* O157:H7 among 27 infected herds (adapted from Hancock et al. 1997b).

The exponential distribution has one parameter, β, that is both its mean and standard deviation. A comparison of the Hancock et al. (1997b) data to predictions from an exponential distribution with $\beta = 1.9\%$ shows general agreement (Figure 3-4). Using a Chi-square statistic, the hypothesis that the observed and expected results were equivalent was not rejected ($\chi^2 = 0.92$, $p>0.05$). Degrees of freedom for this test were determined using Scott's normal approximation (Vose 1996).

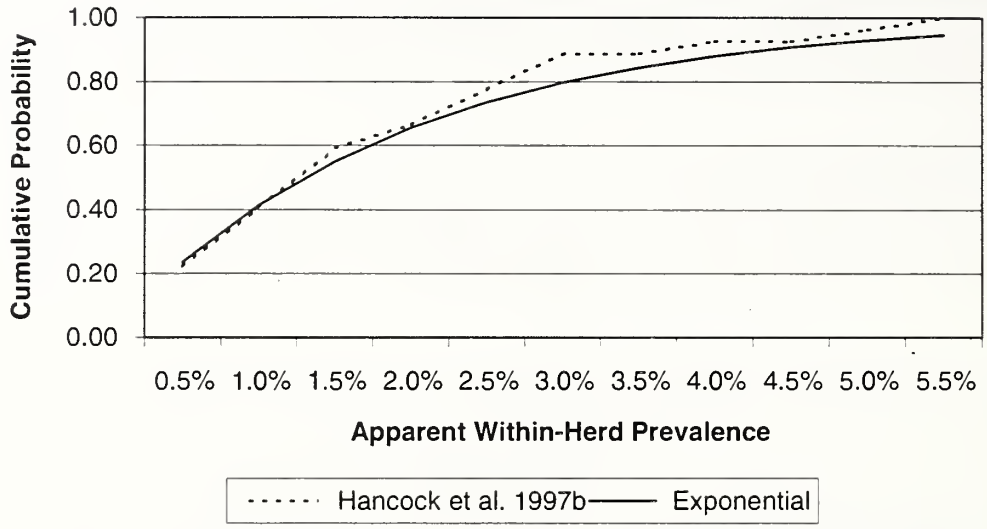

FIGURE 3-4 Comparison of observed and expected cumulative probabilities for within-herd prevalence of *E. coli* O157:H7.

Figure 3-5 is a histogram of within-herd prevalence from a national USDA survey of dairy cows (Garber et al. 1999). These data also reasonably fit an exponential distribution (χ^2 = 9.2, p>0.05) (Figure 3-6).

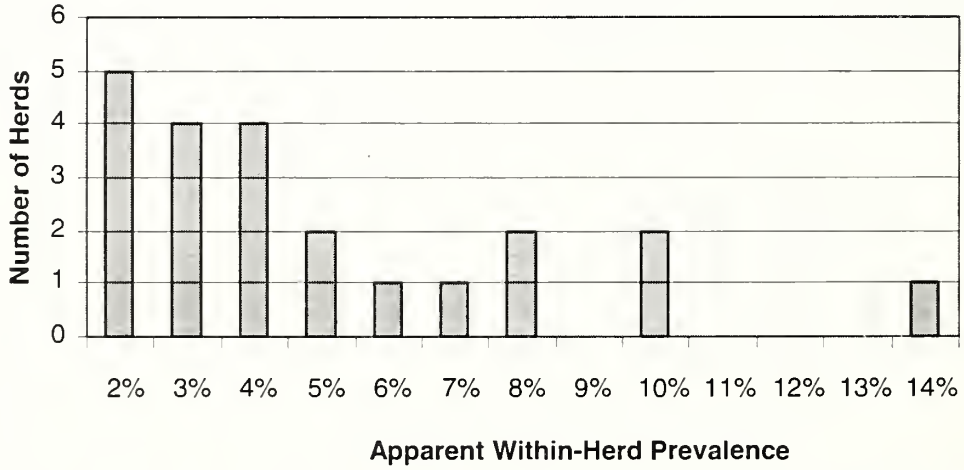

FIGURE 3-5 Evidence on the distribution of within-herd prevalence of *E. coli* O157:H7 among 22 infected herds (adapted from Garber et al. 1999).

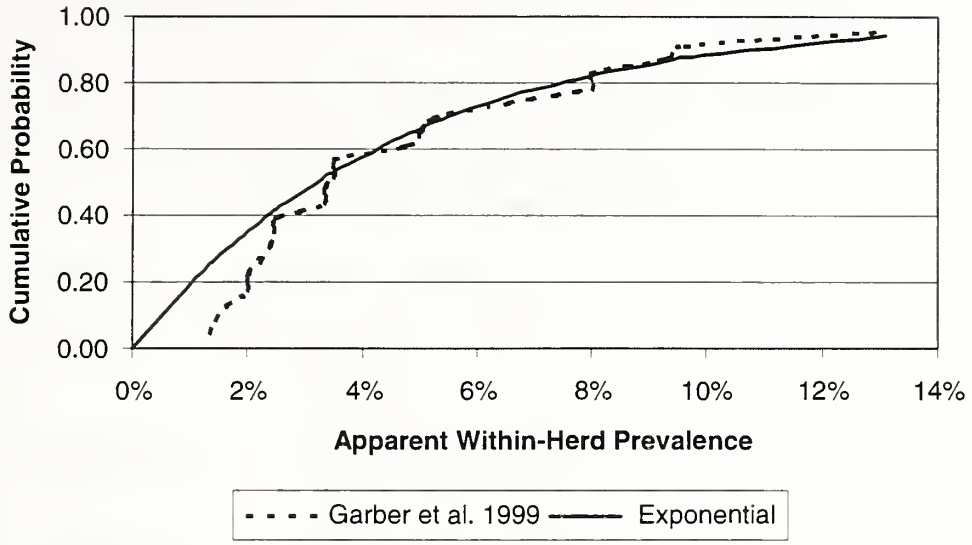

FIGURE 3-6 Comparison of observed and expected cumulative probabilities for within-herd prevalence of *E. coli* O157:H7.

Other prevalence studies either sampled very few infected herds (e.g., Besser et al. 1997; Hancock et al. 1994; Sargeant et al. 2000) or did not collect many samples within each infected herd (Rice et al. 1997). A histogram of within-herd prevalence generated from these studies would not adequately depict its variability. Yet by assuming that within-herd prevalence of *E. coli* O157:H7 fits an exponential distribution, the results from these studies can be used to estimate the average within-herd prevalence. The exponential distribution then describes the variability of within-herd prevalence based on this average.

Seasonal variability. Evidence of a summer peak in cattle *E. coli* O157:H7 prevalence (Hancock et al. 1994; Garber et al. 1999; Hancock et al. 1997a; Heuvelink et al. 1998; Van Donkersgoed et al. 1999) suggests that the greatest *E. coli* O157:H7 prevalence occurs between June and September. It is thought that a summer rise in prevalence results from on-farm environmental conditions that provoke increased transmission of *E. coli* O157:H7 among cattle (Hancock 2001). For example, if feed and water are important in the transmission of *E. coli* O157:H7 to cattle within a herd, then summer ambient temperatures might induce substantial growth of *E. coli* O157:H7 in the feed and water that cattle ingest and result in more infected cattle.

One study of cattle in Canada found at least a fourfold difference in *E. coli* O157:H7 fecal prevalence between samples collected in the winter and summer (Van Donkersgoed et al. 1999). The greatest fecal prevalence was observed between June and August. In a national study of U.S. dairies, herds sampled between May and July were nearly eight times more likely to be fecal positive than those sampled between February and April (Garber et al. 1999). Longitudinal studies that followed the same infected herds for a full year have found a three- to sixfold difference in prevalence between winter and summer (Hancock et al. 1997a; Heuvelink et al. 1998). Nevertheless, a yearlong study of 10 cow-calf herds did not demonstrate any seasonal difference in prevalence (Sargeant et al. 2000).

To model the effect of season, within-herd prevalence is estimated for two periods: June to September, which constitutes the high prevalence season, and the other months of the year, which constitute the low prevalence season. Each season's average within-herd prevalence is

estimated. During each season, population variability of within-herd prevalence is modeled via the exponential distribution.

Evidence of Apparent Within-Breeding Herd Prevalence

Six studies provide evidence on apparent within-herd prevalence of infected adult cattle in U.S. breeding herds (Table 3-2). Although all of these studies sampled adult cows and bulls, the study design, sampling scheme, and culturing methods often differed.

TABLE 3-2 Evidence Used to Estimate Within-Herd Prevalence of *E. coli* O157:H7 in Breeding Herds

Study	Number Tested in Positive Herds	Positive in Positive Herds	Apparent Within-Herd Prevalence	Lab Methods	Months Sampled
Hancock et al. 1994	458	20	4.4%	0.1 g, SMAC	June–July, September
Besser et al. 1997	2074	53	2.6%	0.1 g, SMACct	January–December
Rice et al. 1997	75	7	9.3%	0.1 g, SMACct	July–December
Garber et al. 1999	1268	51	4.1%	1 g, SMACct, TSB	February–July
Sargeant et al. 2000	2348	29	1.2%	10 g, IMS	January–December
Hancock et al. 2001	5709	38	0.7%	0.1 g, SMACct	December–March, June–September

Note: g = grams of feces analyzed,
SMAC = sorbitol MacConkey media,
SMACct = sorbitol MacConkey media with cefixime and tellurite,
TSB = trypticase soy broth, and
IMS = immunomagnetic separation.

Hancock et al. (1994) surveyed 25 cow-calf herds in Washington, and 4 (16%) were positive. Within those positive herds, about 4% of cows were fecal positive for *E. coli* O157:H7. Sampling was conducted in June, July, and September 1992.

Besser et al. (1997) conducted a yearlong study of 10 dairy herds in Washington, and 4 (40%) were positive. Within those positive herds, the prevalence of positive cattle was about 3%. Sampling was completed during 1993 and 1994.

Rice et al. (1997) sampled cows culled from 13 positive dairy herds in Idaho, Oregon, and Washington. This study found 9% of cattle from positive herds to be fecal positive. Sampling was conducted between July and December 1994.

In Garber et al. (1999), 22 infected dairy herds were detected as part of a national USDA survey. Four percent of the cows sampled in the positive herds were *E. coli* O157:H7-positive. Sampling was conducted between February and July 1996.

Sargeant et al. (2000) detected 10 positive Kansas cow-calf herds in a yearlong study. About 1% of the cows were fecal positive. The study was conducted between December 1996 and December 1997.

Hancock et al. (2001) are completing a study in which 18 positive herds have been detected. Almost 1% of cattle sampled in positive herds are positive. These results reflect sampling conducted during 2000 and 2001.

True within-herd prevalence can be estimated from apparent within-herd prevalence (Martin et al. 1987):

$$\text{True Prevalence} = \frac{\text{Apparent Prevalence}}{\text{Test Sensitivity}} \tag{3.5}$$

Apparent prevalence is estimated as a beta(s+1,n–s+1), where s is the number of test positive cattle in a study and n is the total cattle tested in positive herds (Vose 1996). Test sensitivity is estimated from research evidence.

Test Sensitivity

The probability of observing a positive biological test result depends on test sensitivity. Both the culture methods used and the quantity of sample collected affect test sensitivity. The absolute sensitivity of microbiological tests applied to naturally-infected cattle has not been established because there is no suitable "gold" standard for determining the true infection status of cattle. Nevertheless, Sanderson et al. (1995) have evaluated the sensitivity of culturing methods using 24 naturally-infected dairy cattle (Table 3-3). These relative sensitivity measures included the effects of different culture methods and sample quantities. The least sensitive method had a relative sensitivity of 0.33—in other words, only 33% of the infected cattle were found positive using this method. The most sensitive method had a relative sensitivity of 0.79.

TABLE 3-3 Relative Test Sensitivity of Lab Methods. Twenty-four test-positive cattle were detected using different sample quantities (0.1 gram and 10 grams) and plating media.

Lab Methods	Number Positive	Relative Sensitivity
0.1 gram, TSBcv, SMACc	8	0.33
0.1 gram, TSBcv, SMACct	14	0.58
10 gram, TSBcv, SMACct	19	0.79
Total positives	24	

Note: TSBcv = trypticase soy broth with cefixime and vancomycin,
SMACc = sorbitol MacConkey media with cefixime, and
SMACct = sorbitol MacConkey media with cefixime and tellurite.

Source: Adapted from Sanderson et al. 1995.

The quantity of feces sampled from cattle influences test sensitivity because infected cattle shed *E. coli* O157:H7 in varying concentrations. Variability in *E. coli* O157:H7 fecal concentration from naturally-infected cattle has been reported (Zhao et al. 1995; Cassin et al. 1998). The range of feasible concentrations should extend to 10^7 to account for shedding levels infrequently observed in experimentally-infected adult cattle (Cray and Moon 1995). A minimum shedding concentration of 10^{-1} colony-forming units (CFU) per gram of feces can be assumed, based on a 10-gram sample. Plausible frequencies for this range of fecal concentrations are listed in Table 3-4.

TABLE 3-4 Calculation of the Probability of Detecting One or More Organisms Given the Sample Quantity, Concentration of Organisms per Gram of Feces, and Frequency (f[x]). Lambda (λ) equals the CFU per gram multiplied by the sample size. The sum of each column is the expected frequency of samples containing no *E. coli* O157:H7 organisms from a cross-section of infected cattle.

		$P(x=0\|\lambda)*f(x)$		
CFU per Gram of Feces	f(x)	0.1 Gram Sample	1 Gram Sample	10 Gram Sample
0.1	0.12	0.117	0.107	0.043
1	0.12	0.107	0.043	0.000
10	0.12	0.043	0.000	0.000
100	0.12	0.000	0.000	0.000
1,000	0.06	0.000	0.000	0.000
10,000	0.35	0.000	0.000	0.000
100,000	0.09	0.000	0.000	0.000
1,000,000	0.02	0.000	0.000	0.000
10,000,000	0.01	0.000	0.000	0.000
Sum	1	0.267	0.150	0.043
1–Sum		0.733	0.850	0.957

Fecal prevalence studies have included 0.1-gram, 1-gram, and 10-gram sample quantities. The probability that a given sample quantity will not contain any organisms is predicted by the Poisson distribution, e^{-xz}, where x is concentration per gram of feces and z is the sample quantity in grams. If x is a distribution, then this probability is the expected value across all concentrations (i.e., $\Sigma f(x) \times e^{-xz}$), where f(x) is the frequency of concentration x.

The probability of a sample containing one or more organisms is equal to one minus the probability it contains no organisms. The probability that a sample size of 0.1, 1.0, and 10 grams will contain at least one organism is 0.73, 0.85, and 0.96, respectively (Table 3-4). Therefore, increasing the sample quantity from 0.1 grams to 10 grams results in 23% (= 96% – 73%) more samples with 1 or more *E. coli* O157:H7 organisms from infected cattle. Interestingly, when 0.1- and 10-gram samples were evaluated using the same enrichment and plating system (i.e., TSBcv, SMACct), the 10-gram sample detected 79% of infected cattle while the 0.1-gram sample detected 58% of these cattle, a difference of 21% (Table 3-3). Therefore, the observed difference in sensitivity between these methods approximates the effect of different sample quantities.

The test sensitivity applicable to the Besser et al. (1997), Rice et al. (1997), and Hancock et al. (2001) studies is shown in Table 3-3 (i.e., 0.58). The other within-herd prevalence studies used alternative methods for which test sensitivity is not directly reported.

The Garber et al. (1999) study used 1.0-gram samples and TSB-SMACct. Neither the TSB enrichment nor the 1.0-gram sample size is available from the results in Table 3-3. The TSBcv-SMACct culturing protocol detected 80% of samples experimentally spiked with *E. coli* O157:H7 (Sanderson et al. 1995). Yet a 1.0-gram sample from infected cattle is only 85% likely to contain *E. coli* O157:H7. Therefore, a 1.0-gram, TSBcv-SMACct protocol is predicted to detect 68% (85% × 80%) of infected cattle. In another experiment, the difference between the

TSB enrichment system and the TSBcv system equaled –10% (Sanderson et al. 1995). Therefore, the sensitivity for the 1.0-gram TSB-SMACct sampling protocol is estimated as 58%.

Hancock et al. (1994) used 0.1-gram samples and TSBv-SMAC. The SMAC plating system only detected 3% of samples experimentally spiked with *E. coli* O157:H7 (Sanderson et al. 1995). A 0.1-gram sample from infected cattle is only 73% likely to contain *E. coli* O157:H7. Therefore, the sensitivity of the 0.1 gram-TSBv-SMAC sampling protocol was estimated as 2% (73% × 3%).

Sargeant et al. (2000) used 10-gram samples and immunomagnetic separation (IMS) with microbiologic culture to improve the detection of *E. coli* O157:H7 in fecal samples. The IMS process was found to have a sensitivity that was 20% greater than a single dilution microbiologic culture system (Sanderson et al. 1995). Therefore, sensitivity of the 10-gram IMS sampling protocol was estimated as 100%.

Test sensitivities in Table 3-3 and those generated above were used in Equation 3.5 to estimate true prevalence. Uncertainty regarding test sensitivity was modeled using beta distributions (Vose 1996).

True Within-Breeding Herd Prevalence

Seasonal variability. Examining the monthly prevalence evidence, there appears to be a high prevalence season (June to September) and a low prevalence season (October to May).

Three studies (Garber et al. 1999; Hancock et al. 1994, 2001) provide different sampling evidence for different months of the study. For example, Garber et al. (1999) sampled cattle from February through July. These data show that 7 of 193 cattle sampled in infected herds were fecal positive during the period from February to May. In contrast, 44 of 1,075 cattle sampled in infected herds during June and July were fecal positive.

Data collected for each month of the year were pooled. Prior to pooling, true within-herd prevalence for each study was estimated. Average within-herd prevalence was calculated for each month across all the applicable studies by weighting each study by the average cattle sampled per month in the study. Within-herd prevalence estimated for June to September was averaged to calculate within-herd prevalence during the high prevalence season. Similarly, within-herd prevalence during the low prevalence season was the average across October to May.

Table 3-5 illustrates this method of estimating seasonal averages using point estimates. Recall that true prevalence is a random variable estimated from two beta-distributed variables (apparent prevalence and test sensitivity). These point estimates illustrate one scenario when the averages of apparent prevalence and test sensitivity are used. To calculate true averages, Monte Carlo methods were used to simulate the underlying distributions (Haas et al. 1999).

Figure 3-7 overlays a centered 3-month moving average curve upon nine illustrative iterations of the Monte Carlo model. The moving average curve is calculated from 1,000 iterations of the model and demonstrates a seasonal pattern of within-herd prevalence. Nevertheless, the limited data and estimation method also result in considerable uncertainty about the true monthly within-herd prevalence. A given month's estimate may be substantially influenced by the amount of available data (e.g., August) as well as the uncertainty in apparent prevalence and test sensitivity. Nevertheless, the volatility implied by the single iteration curves is dampened because the model only considers estimates of the high and low prevalence seasons.

Figure 3-8 shows the uncertainty about the seasonal averages. Despite the apparent overlap of the two seasonal distributions, there were 913 of 1,000 iterations of the Monte Carlo model in which the prevalence for June to September (high prevalence season) was greater than that for

TABLE 3-5 Point Estimates for Monthly True Within-Herd Prevalence for Each of Six Studies (Table 3-2). A weighted average for each month was calculated (based on average numbers of samples collected per month per study), and a seasonal average was calculated for the high and low prevalence seasons.

	Weighted Average						
Month	Hancock et al. 1994	Besser et al. 1997	Rice et al. 1997	Garber et al. 1999	Sargeant et al. 2000	Hancock et al. 2001	Average
January		4.5%			1.3%	1.0%	1.6%
February		4.5%		7.1%	1.3%	1.0%	2.6%
March		4.5%		7.1%	1.3%	1.0%	2.6%
April		4.5%		7.1%	1.3%		4.6%
May		4.5%		7.2%	1.3%		4.6%
June	45.3%	4.5%		7.2%	1.3%	1.4%	4.2%
July	66.8%	4.5%	18.0%	7.2%	1.3%	1.4%	5.0%
August		4.5%	18.0%		1.3%	1.4%	2.1%
September	75.6%	4.5%	18.0%		1.3%	1.4%	4.8%
October		4.5%	18.0%		1.3%		3.3%
November		4.5%	18.0%		1.3%		3.3%
December		4.5%	18.0%		1.3%	1.0%	1.7%
Weights	46	173	13	254	196	794	
October–May average		(low prevalence season)			3.0%		
June–September average		(high prevalence season)			4.0%		
January–December average					3.4%		

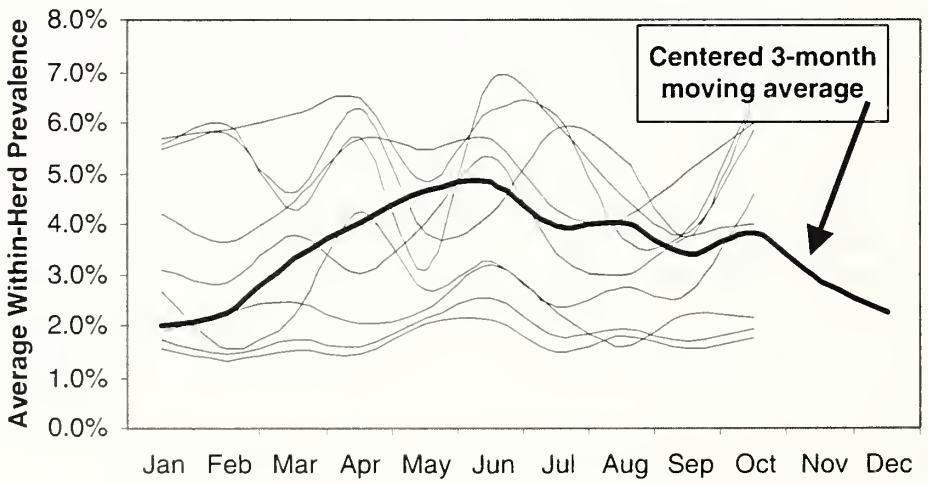

FIGURE 3-7 Estimated average monthly within-herd prevalence. This illustrated seasonal trend is based on 1,000 iterations of the model.

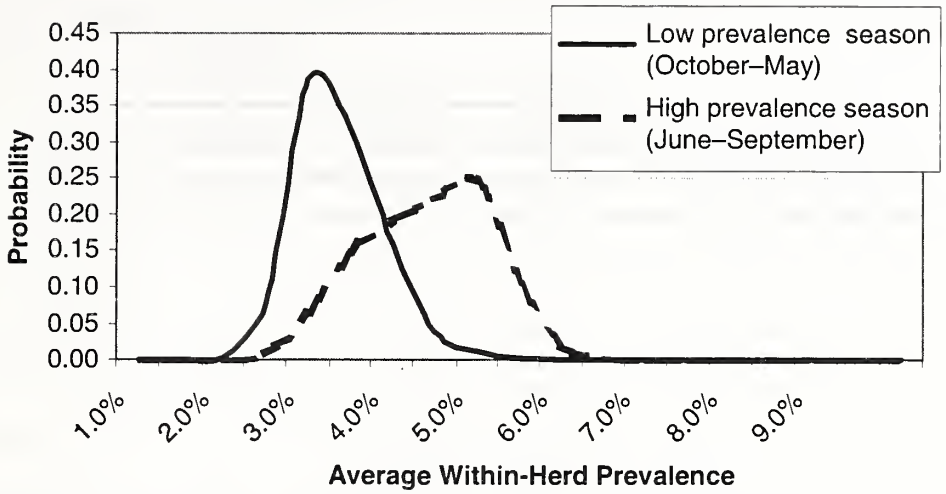

FIGURE 3-8 Uncertainty about low and high prevalence seasons' estimated average within-herd prevalence. These distributions were estimated using 1,000 Monte Carlo iterations of the model.

the rest of the year (low prevalence season). The averages of the low and high prevalence season distributions were 3.1% and 4.2%, respectively. Therefore, this analysis suggests that within-herd prevalence is increased 33% during June to September relative to the rest of the year. For comparison, the Sargeant et al. (2000) study found no evidence of change by season, and the Hancock et al. (2001) study found a 66% increase during June to September. These studies sampled adult cows during both the low and high prevalence seasons.

These results imply that prevalence within infected breeding herds during June to September varies around a greater average than during other months of the year. Consequently, cattle shipped to slaughter from infected herds during June to September are more likely to be infected than at other times. If cattle slaughtered during June to September are more likely to be infected, then the risk associated with ground beef produced from these cattle may also be elevated relative to other times of the year.

Feedlot Prevalence

As with breeding herds, the prevalence of infected feedlots is also assumed to be constant across time. The occurrence of *E. coli* O157:H7 in feedlots does not show any geographic clustering (Hancock et al. 1998b, 2001). Therefore, U.S. feedlot prevalence data are also pooled without regard for the region where the data were collected.

Apparent Feedlot Prevalence

Four studies provide evidence regarding the apparent prevalence of infected feedlots (Table 3-6). Feedlots sampled in each study came from multiple states.

Dargatz et al. (1997) report on a national survey conducted by USDA in 1994 (Hancock et al. 1997c). In this study, 100 feedlots were randomly selected throughout the United States; 63 feedlots were found to contain one or more positive cattle. Thirty fecal samples per pen were collected from four pens in each feedlot. About 3% of cattle sampled in positive feedlots were fecal positive.

TABLE 3-6 Evidence Used to Estimate Feedlot Prevalence

Study	Feedlots Tested	Positive Feedlots	Apparent Feedlot Prevalence	Average Samples per Feedlot	Apparent Within-Feedlot Prevalence	Lab Methods	Months Sampled
Dargatz et al. 1997	100	63	63%	120	3%	0.1 g, SMACct	October–December
Hancock et al. 1998b	6	6	100%	174	4%	0.1 g, SMACct	July–November
Smith 1999	5	5	100%	611	23%	10 g, IMS	June–September
Elder et al. 2000	29	21	72%	12	36%	10 g, IMS	July–August

Note: g = grams of feces analyzed,
SMACct = sorbitol MacConkey media with cefixime and tellurite, and
IMS = immunomagnetic separation.

Hancock et al. (1998b) completed a survey of six feedlots in Idaho, Oregon, and Washington during 1996. At least one positive cattle was detected in each feedlot. An average of 174 samples were collected per feedlot, and about 4% of cattle in positive feedlots were positive.

Smith (1999) sampled five midwestern feedlots, and all were found to contain positive cattle. Four to five pens were intensively sampled in each feedlot during a 3-month period during summer 1999. An average of 611 samples were collected per feedlot, and 23% of cattle in these feedlots were positive. This study used much more sensitive test methods than the previous studies.

Elder et al. (2000) also used very sensitive test methods to sample cattle at four midwestern slaughter plants in 1999. It was assumed that each lot of cattle sampled in this study represented a pen of cattle originating from a randomly selected feedlot. Of the 29 lots sampled, 21 were detected to contain one or more positive cattle. While an average of only 12 samples were collected per lot, 36% of the cattle were *E. coli* O157:H7-positive in positive lots.

True Feedlot Prevalence

To estimate true feedlot prevalence, the same methods were used as described for breeding herd prevalence (Equations 3.1 to 3.4). Herd sensitivity (HSens) was estimated to be 0.77, 0.86, 0.99, and 0.81 based on analysis of the Dargatz et al. (1997), Hancock et al. (1998b), Smith (1999), and Elder et al. (2000) studies, respectively.

Figure 3-9 shows the estimated distribution for true feedlot prevalence. This distribution suggests that feedlot prevalence is most likely 90%, but it may be as low as 70% or as high as 100%.

These results imply that most, if not all, U.S. feedlots contain one or more *E. coli* O157:H7-infected cattle. Such a result is not surprising given the management—and high turnover rate—of cattle in feedlots. Cattle entering feedlots are typically confined in pens, fed from common feed bunks, and usually shipped to slaughter 3 to 6 months after arrival. Also, feedlot cattle usually originate from multiple locations. Therefore, feedlots hypothetically provide ample opportunity for exposure and transmission of *E. coli* O157:H7 to cattle. The elevated feedlot prevalence estimate from this risk assessment supports such a hypothesis.

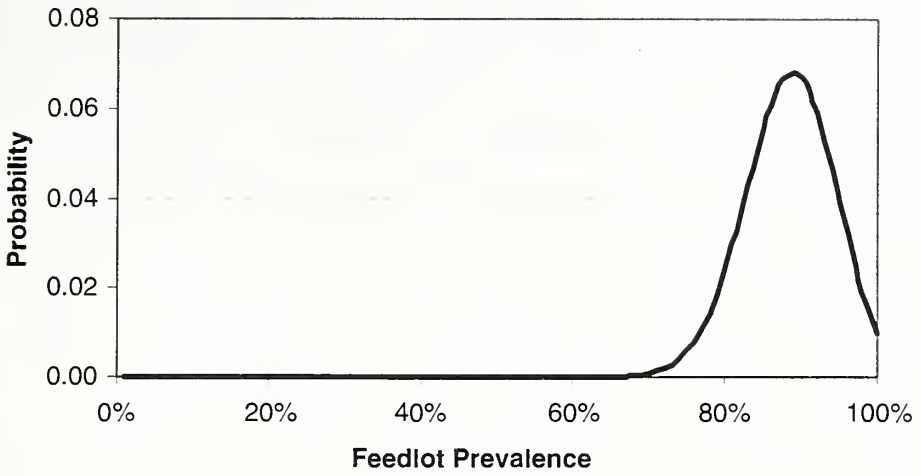

FIGURE 3-9 Resultant uncertainty distribution for true feedlot prevalence after analysis of data in Table 3-6.

Within-Feedlot Prevalence

Within-feedlot prevalence is estimated using the same methods employed for breeding herds.

Apparent Within-Feedlot Prevalence

Population variability. Like within-breeding herd prevalence, within-feedlot prevalence also varies. Figure 3-10 shows the apparent within-feedlot prevalence distribution for 63 infected feedlots (Dargatz et al. 1997). This study included the greatest number of infected feedlots of any published report on U.S. feedlots.

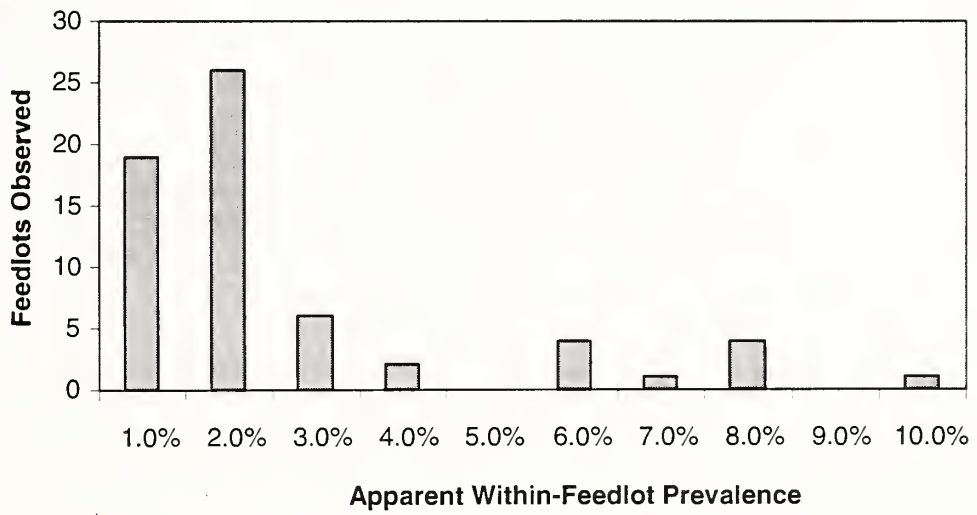

FIGURE 3-10 Evidence on the distribution of within-feedlot prevalence of *E. coli* O157:H7 in infected feedlots (adapted from Dargatz et al. 1997).

As discussed previously, this asymmetric distribution plausibly fits an exponential distribution. The mean and standard deviation of this distribution are 2.7% and 2.2%, respectively. A comparison of this distribution to predictions from an exponential distribution with $\beta = 2.7\%$ also shows some agreement (Figure 3-11). Nevertheless, the hypothesis that the observed and expected results are equivalent is rejected ($\chi^2 = 18.9$, $p<0.05$).

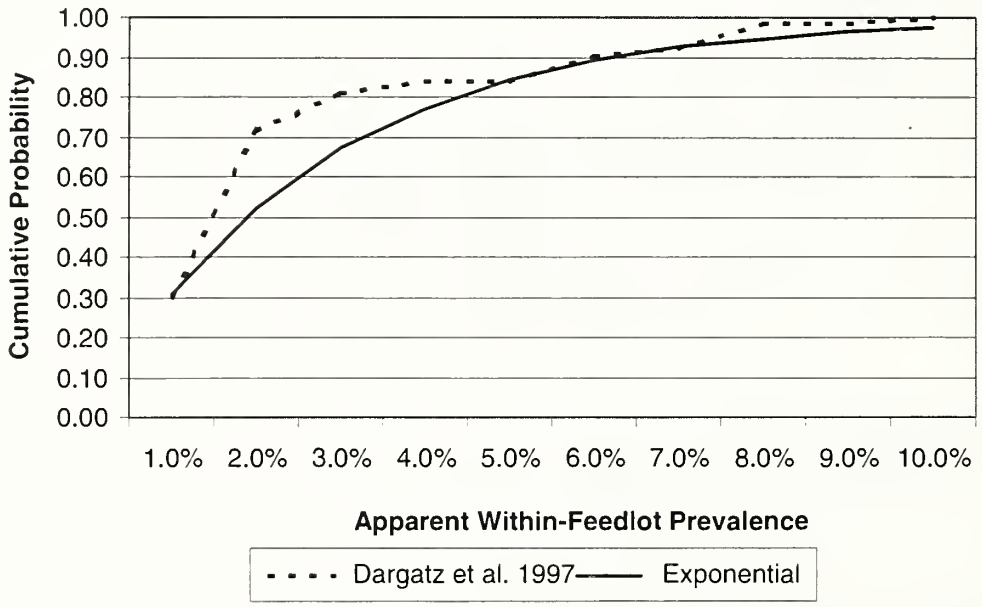

FIGURE 3-11 Comparison of observed and expected cumulative probabilities for within-feedlot prevalence of *E. coli* O157:H7.

Despite the lack of statistical support to conclude that these data fit an exponential distribution, it is assumed that within-feedlot prevalence can be adequately represented with such a distribution. As with breeding cattle studies, most available feedlot data only allow estimation of average within-feedlot prevalence. Therefore, fitting these other data to more complex parametric distributions (e.g., lognormal) is not feasible.

When available data are limited to averages, the principle of Maximum Entropy supports the use of an exponential distribution (Vose 1996). This distribution choice is likely conservative because disagreement between the observed and theoretic distributions tends to occur at lower prevalence levels. Nevertheless, because within-herd prevalence was shown to fit an exponential distribution, such a distribution seems biologically plausible.

Seasonal variability. Most studies of feedlot cattle were completed over limited times of the year. Therefore, evidence of a summer season peak in prevalence is limited for this class of cattle. One Canadian study, which included fed steers and heifers, showed peak prevalence in the summer (Van Donkersgoed et al. 1999). Most U.S. studies completed between June and September report higher *E. coli* O157:H7 prevalence levels than studies completed at other times of the year.

Seasonal variability in within-feedlot prevalence is modeled using the same methods as applied to within-breeding herd prevalence. Although the epidemiology of *E. coli* O157:H7 in cattle is not completely characterized, it seems unlikely that factors (e.g., feed or water

contamination) associated with increased transmission in the warm summer months in breeding cattle are different for feedlot cattle.

Evidence of Apparent Within-Feedlot Prevalence

Five studies provide evidence on apparent within-feedlot (Table 3-7). Dargatz et al. (1997) detected 63 positive feedlots in a national USDA survey. The prevalence of *E. coli* O157:H7-positive cattle in positive feedlots was about 3%. Sampling was conducted between October and December 1994.

TABLE 3-7 Evidence Used to Estimate Within-Feedlot Prevalence

Study	Number Tested in Positive Feedlots	Positive in Positive Feedlots	Apparent Within-Feedlot Prevalence	Lab Methods	Months Sampled
Dargatz et al. 1997	7,560	210	2.8%	0.1 g, SMACct	October–December
Hancock et al. 1998b	1,046	38	3.6%	0.1 g, SMACct	July–November
Hancock et al. 1999	240	14	5.8%	0.1 g, SMACct	November–January, May–June
Smith 1999	3,054	707	23.1%	10 g, IMS	June–September
Elder et al. 2000	254	91	35.8%	10 g. IMS	July–August

Note: g = grams of feces analyzed,
SMACct = sorbitol MacConkey media with cefixime and tellurite, and
IMS = immunomagnetic separation.

Hancock et al. (1998b) found six positive feedlots in three northwestern states. The apparent within-feedlot prevalence was 4%. This study was completed between July and November 1996.

Hancock et al. (1999) studied the prevalence of *E. coli* O157:H7 in the feces of steers and heifers from eight lots at four slaughter plants. When sampling was done just after the cattle were stunned in the slaughter plant, 5.8% of 240 cattle were reported positive. Sampling was conducted in November 1995 to January 1996, and May to June 1996.

Smith (1999) found five positive midwestern feedlots that contained large numbers of positive cattle. The reported apparent within-feedlot prevalence was 23%. The study was conducted from June to September 1999.

Elder et al. (2000) sampled cattle at four midwestern slaughter plants and found 21 positive lots. Within those lots, the prevalence of test-positive cattle was about 36%. This study was conducted in July and August 1999.

Three of these studies used the same sampling and lab methods (Dargatz et al. 1997; Hancock et al. 1998b, 1999). These methods are reportedly 58% sensitive (Sanderson et al. 1995). In contrast, the other studies collected 10-gram samples and used an IMS process followed by microbiologic culture to improve the detection of *E. coli* O157:H7 in fecal samples. As explained previously, this protocol is assumed to be 100% sensitive.

True Within-Feedlot Prevalence

True within-feedlot prevalence data were organized by study months (Table 3-8). No empirical evidence was available between February and April. Therefore, prevalence for these months was calculated using moving averages from the 3 preceding months.

TABLE 3-8 Point Estimates for Monthly True Within-Feedlot Prevalence for Each of Five Studies (Table 3-6). A weighted average for each month was calculated (based on average numbers of samples collected per month per study), and a seasonal average was calculated for the high and low prevalence seasons.

	Weighted Average					
Month	Dargatz et al. 1997	Hancock et al. 1998b	Hancock et al. 1999	Smith 1999	Elder et al. 2000	Average
January			18%			18%
February						10%
March						11%
April						13%
May			4%			4%
June			4%	24%		23%
July		6%		24%	37%	22%
August		6%		24%	37%	22%
September		6%		24%		20%
October	5%	6%				5%
November	5%	6%	18%			5%
December	5%		18%			5%
Weights	2,520	209	48	764	127	
October–May average		(low prevalence season)		9%		
June–September average		(high prevalence season)		22%		
January–December average				13%		

Figure 3-12 illustrates nine random iterations of a Monte Carlo model estimating monthly within-feedlot prevalence. A strong seasonal peak is evident from this graph and is consistent from iteration to iteration.

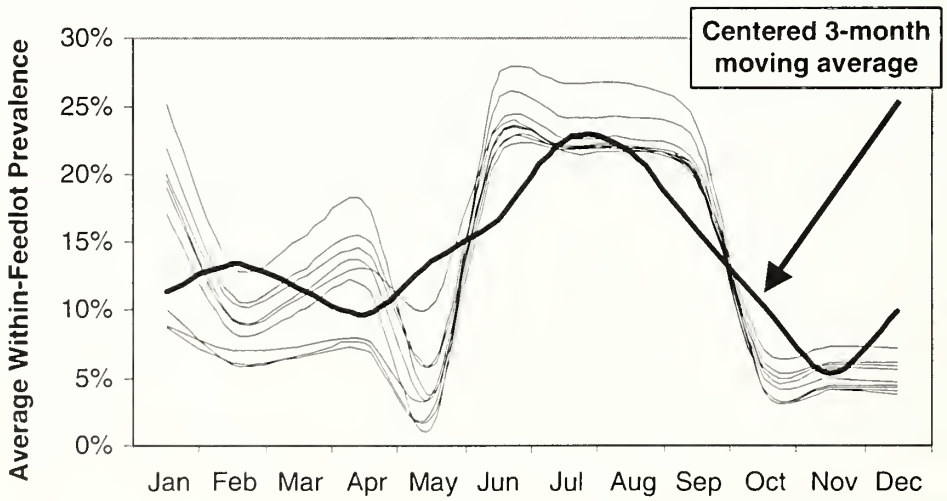

FIGURE 3-12 Estimated average monthly within-feedlot prevalence. This illustrated seasonal trend is based on 1,000 iterations of the model.

Figure 3-13 shows the uncertainty about the low and high prevalence seasonal averages. The mean within-feedlot prevalence is 9% and 22% for the low and high prevalence seasons, respectively. In contrast to the breeding herd analysis (Figure 3-8), the two seasonal distributions are distinctly different, and there is more than a twofold difference between the low and high prevalence seasons for feedlots.

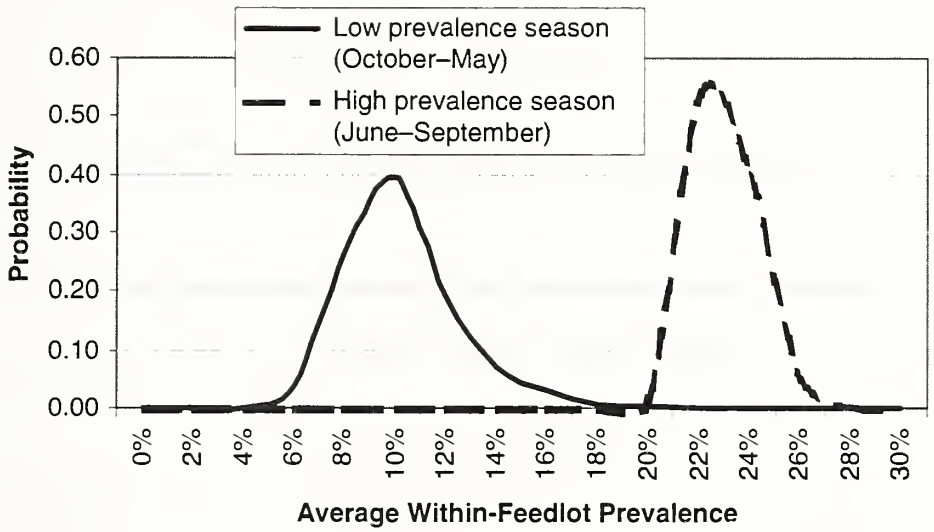

FIGURE 3-13 Uncertainty about low and high prevalence seasons' estimated average within-feedlot prevalence. These distributions were estimated using 1,000 Monte Carlo iterations of the model.

These results imply that within-feedlot prevalence is greater than within-breeding herd prevalence. This difference may be related to cattle age. Feedlot cattle age is typically less than 1 year, while breeding cattle age is over 2 years. A higher prevalence of infection in younger cattle has been previously demonstrated (Hancock et al. 1994; Dargatz et al. 1997; Mechie et al. 1997; Heuvelink et al. 1998; Van Donkersgoed et al. 1999). Acquired or natural immunity may increase with cattle age and result in increased resistance to infection by older cattle. Regardless of cause, the differences in within-feedlot and within-breeding herd prevalence seem consistent with the available evidence.

These results also show that within-feedlot prevalence increases substantially during June to September. At all times of the year, feedlot cattle sent to slaughter are more likely than breeding cattle to be infected. Yet this discrepancy is greatest during the high prevalence season. While there are differences in management between feedlots and breeding herds, the available data do not explain why the seasonal peak is much greater for feedlots than for breeding herds.

Transportation Segment

Transmission of *E. coli* O157:H7 from infected to susceptible cattle may occur when cattle are transported to slaughter. Alternatively, some infected cattle may rid themselves of infection during the period they are being shipped to slaughter. This segment addresses the effect of transportation on prevalence of *E. coli* O157:H7 in feces and hides.

Transportation Effects on Fecal Prevalence

Empirical evidence suggests that there is no dramatic difference in fecal prevalence between the farm and slaughter plant. Rice et al. (1997) collected fecal samples of culled dairy cattle both at the farm and at slaughter. Of 205 samples collected at the farm, 3.4% were *E. coli* O157:H7-positive. Of 103 samples collected at slaughter, 3.9% were *E. coli* O157:H7-positive. Of 89 paired samples (farm and slaughter), 2.2% were positive at both the farm and slaughter, 3.3% were positive at the farm only, and 2.2% were positive at slaughter only.

In a study of New York cull cows (Cornell 1998), 1.3% of 3,323 cull dairy cows were fecal positive for *E. coli* O157:H7 at a slaughter plant. No difference in the average transit time was found between *E. coli* O157:H7-positive cattle and *E. coli* O157:H7-negative cattle (32.6 and 31.7 hours, respectively). Therefore, duration of transportation was not associated with being fecal positive.

In a national study of dairy cattle, 2.8% of approximately 600 cows to be culled within the subsequent 7 days were fecal positive for *E. coli* O157:H7 (APHIS-VS-NAHMS 1998). This study also collected fecal samples from over 2,200 dairy cows at livestock markets across the country and found 1.8% of these animals *E. coli* O157:H7-positive.

The data do not suggest that *E. coli* O157:H7 prevalence increases during transport to slaughter. Therefore, no effect from transport is included in the model.

Feedlot cattle are typically shipped directly to slaughter and processed the same day. Therefore, it is reasonable that prevalence is unaffected by transport of this class of cattle. On the other hand, culled breeding cattle are more likely to be shipped to slaughter via livestock markets. This marketing route seemingly increases the elapsed time for shipment. If *E. coli* O157:H7 is transmitted to susceptible cattle during this transport time, the evidence suggests that infected cattle are ridding themselves of infection at a rate equivalent to the transmission rate. In this case, prevalence after shipping remains the same as prevalence before shipping.

Transportation Effects on Hide Contamination

Transit between the farm and slaughter plant may be important in causing changes in hide prevalence. Studies of hide contamination with *Salmonella* suggest an increase in prevalence of hide-contaminated cattle between the farm and slaughter (Puyalto et al. 1997; Cornell 1998).

Data are limited on *E. coli* O157:H7 hide-contaminated cattle. In one study, 1.7% of 240 feedlot cattle at four slaughter plants had hair samples that were *E. coli* O157:H7-positive (Hancock et al. 1999). Paired fecal samples were collected from the animals in this study, and no correspondence between fecal and hide status was found. Elder et al. (2000) collected nonpaired fecal and hide samples from cattle at four slaughter plants. Average fecal prevalence was 28%, yet average hide prevalence was only 11%. Generally, hide-positive lots also contained fecal-positive cattle, but fewer lots were detected from hide sampling. Another study conducted by the American Meat Institute (Bacon et al. 2000) found that 3.6% of 2,245 cattle were hide-positive from samples collected at 12 slaughter plants.

Some researchers hypothesized that the degree of visible soiling of cattle surfaces (e.g., hides, hair) with mud, manure, and/or bedding is correlated with microbial contamination of carcasses (Van Donkersgoed et al. 1997; Jordan 1998). Yet no clear correlation was found. The concentration of *E. coli* Biotype I organisms on carcasses changed very little whether the lot was composed of cattle that had substantial hide soiling or were relatively clean. The implication of this research is that the role of *E. coli* O157:H7 hide contamination in carcass contamination may not be correlated with grossly visible soiling.

Because there are no data on *E. coli* O157:H7 hide-contaminated cattle at the farm and only limited data on hide prevalence at the slaughter plant, the effect of transit time on hide

contamination cannot be examined at this time. The available evidence suggests that fecal prevalence may be a better predictor of carcass contamination than hide prevalence (Elder et al. 2000). If this is the case, then incorporating the effect of hide contamination may be inconsequential. Nevertheless, better hide sampling methods are needed to fully assess the importance of hide prevalence.

Slaughter Plant Intake Segment

Breeding Cattle

Culled dairy and beef cattle arrive at the slaughter plant from their farms of origin after transit on trucks. The majority of these cows and bulls arrive after first being shipped to one or more livestock markets where they are auctioned to the highest bidder and then shipped to slaughter (APHIS:VS:CEAH 1994).

The combined average herd size for dairy and beef herds is approximately 300 cows (NASS 1998). Approximately 25% of cows in dairy herds, and 11% of cows in beef herds, are culled each year (APHIS-VS-NAHMS 1996, 1997). These culling percentages imply that the average herd would ship from 1 to 1.5 cattle per week.

Given the low culling rate per herd, it is reasonable to assume random mixing of breeding cattle at slaughter plants. Such an assumption implies that the prevalence of *E. coli* O157:H7-infected breeding cattle at slaughter is the product of herd prevalence and within-herd prevalence. It also implies that the probability of one cow on the slaughter line being infected is independent of the probability of another cow on the slaughter line being infected. A violation of this assumption would be a group of cows (i.e., 40 cows) from the same farm all sent to slaughter together and then slaughtered one after the other. In this case, the prevalence of infected cows in this group is expected to equal the within-herd prevalence of their herd of origin. Violation of a random mixing assumption is expected to occur rarely.

The number of infected cows and bulls in a group of 40 such animals presented for slaughter was simulated using Monte Carlo techniques. Forty head was a convenient count as it is the capacity of most trucks used to haul cattle to slaughter. Each cow and bull was simulated as an individual. The probability of infection is equal to the product of herd prevalence (H) and average within-herd prevalence (w). The number of infected culled breeding cattle per truckload (B) is simulated as follows:

$$B = \sum_{1}^{40} \text{Binomial}\left[1, H \times \text{Exponential}(w)\right] \tag{3.6}$$

Within-herd prevalence varies in the population and by season. Average within-herd prevalence (w) is therefore greater for cattle shipped to slaughter during June through September than for cattle shipped during the rest of the year (see Figure 3-8). To model population variability, an exponential distribution—whose only parameter is the mean within-herd prevalence (w)—is used. Monte Carlo simulations then estimate the number of infected cows/bulls in truckloads for the low and high prevalence seasons.

Feedlot Cattle

Steers and heifers arrive at slaughter plants after being transported from their feedlot of origin in a tractor-trailer truck with a capacity of about 40 head. Most steers and heifers (over 90%) are shipped directly from the feedlot to slaughter without going through a livestock market (APHIS:VS:CEAH 1994). Furthermore, these cattle are typically slaughtered together in a group,

although they may be mixed during slaughter with one or more truckloads of cattle from other feedlots.

The manner by which feedlot cattle are marketed does not support the assumption of random mixing used for culled breeding cattle. Instead, feedlot cattle are much more likely to be processed at the slaughter plant in a clustered pattern. Cattle within the same truckload will all have the same probability of infection because they originated from the same pen in a feedlot.

The number of infected feedlot cattle per truckload (F) is simulated as follows:

$$F = \text{Binomial}(1,H) \times \text{Binomial}[40,\text{Exponential}(w)] \quad (3.7)$$

Each truckload is independently determined to be from an infected or noninfected feedlot based on feedlot prevalence (H). If the truck is from an infected feedlot, then the number infected in the truckload is determined based on the appropriate seasonal within-feedlot prevalence (w). Within-feedlot prevalence varies according to the exponential distribution.

Production Module Results

The four critical inputs to the production module are herd prevalence, within-herd prevalence, feedlot prevalence, and within-feedlot prevalence of *E. coli* O157:H7. Herd prevalence is the proportion of all breeding herds that contain one or more infected cattle. Feedlot prevalence is similar, but the reference population is U.S. feedlots. Within-herd (or within-feedlot) prevalence is the proportion of infected cattle within a herd (or feedlot), given that the herd contains one or more infected cattle. Within-herd (or within-feedlot) prevalence is a random variable that modulates by season. Given the available data, these inputs are quantitatively determined.

Analysis of available evidence provides average, 5th, and 95th percentile estimates for these inputs (Table 3-9). Generally, these results demonstrate that *E. coli* O157:H7 prevalence is significantly greater for feedlot cattle than for breeding cattle (e.g., the 95th percentile for herd prevalence is less than the 5th percentile for feedlot prevalence). Similar findings apply to comparisons between within-herd and within-feedlot prevalence, regardless of season.

TABLE 3-9 Statistics for Uncertain Parameters in the Production Module

Model Input	5th Percentile	Mean	95th Percentile
Breeding herd prevalence	55%	63%	72%
Feedlot prevalence	78%	88%	97%
Low prevalence season (October to May)			
Average within-herd prevalence	2%	3%	4%
Average within-feedlot prevalence	6%	9%	14%
High prevalence season (June to September)			
Average within-herd prevalence	3%	4%	5%
Average within-feedlot prevalence	21%	22%	24%

E. coli O157:H7 prevalence was lower for adult cattle than for feedlot cattle in a yearlong Canadian slaughter survey (Van Donkersgoed et al. 1999). In that survey, 2% of breeding cattle and 12% of feedlot cattle were fecal positive.

The model's annual predictions are the same as this Canadian survey. Average breeding cattle prevalence at slaughter is 3% for the June to September period and 2% for the rest of the year (63% × 4% and 63% × 3%, respectively). Feedlot cattle prevalence at slaughter is 19% for the June to September period and 8% for the rest of the year (88% × 22% and 88% × 9%, respectively). Therefore, on an annual basis, the model predicts that 2% of breeding cattle—and 12% of feedlot cattle—are *E. coli* O157:H7-infected just prior to slaughter. Because Van Donkersgoed et al. (1999) used very sensitive test methods, the concordance of this model's results with that survey is especially noteworthy.

The production module simulates cattle entering the slaughter process via truckloads. Therefore, prevalence of infection within truckloads is this model's output and the first input to the slaughter module. The prevalence of infected cattle within truckloads influences the level of *E. coli* O157:H7 contamination that occurs during slaughter. Generally, when the prevalence in a truckload is elevated, contamination during slaughter is also elevated.

For breeding cattle, about 45% of truckloads are predicted to have no infected cattle (i.e., 0% prevalence) during the low prevalence season (Figure 3-14). Because of model input uncertainty, confidence limits for 0% prevalence are between 40% and 52% of truckloads. During the high prevalence season, 35% (± 7.5%) of these truckloads are predicted to have no infected cattle. Therefore, truckloads containing infected cattle arrive more frequently at slaughter plants between June and September than at other times of the year.

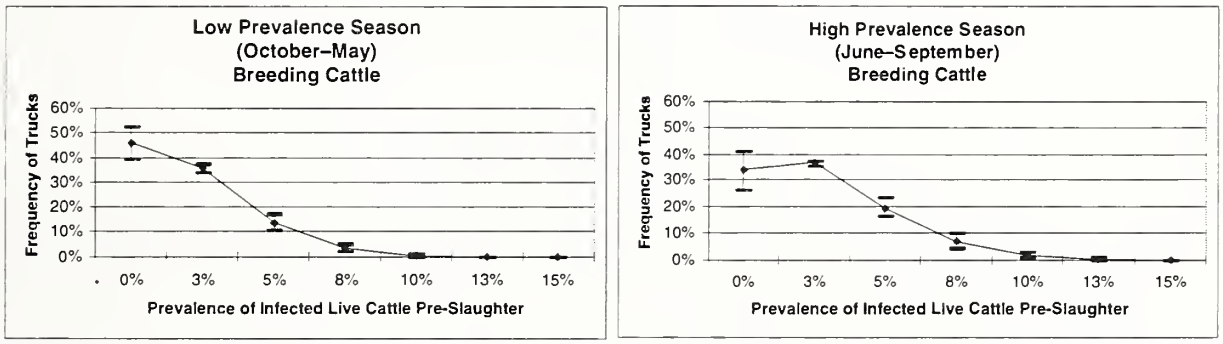

FIGURE 3-14 Comparison of seasonal distributions for prevalence of infected cattle within truckloads of breeding cattle sent to slaughter. Error bars show the 5th and 95th percentiles of uncertainty about frequency of trucks at each prevalence level.

For feedlot cattle, the frequency of truckloads with no infected cattle is about 32% in the low prevalence season and 20% in the high prevalence season (Figure 3-15). Furthermore, there are essentially no trucks with prevalence greater than 30% during the low prevalence season. During the high prevalence season, however, there is a nonnegligible frequency of trucks with greater than 50% prevalence. In fact, there is a 0.1% frequency of trucks with 100% prevalence in the high prevalence season (not shown).

The production model outputs are distributions for cattle prevalence just prior to slaughter. These outputs become the inputs for the slaughter model to follow. The model results predict that feedlot cattle are more likely than breeding cattle to be infected. Furthermore, regardless of cattle type, higher frequencies of infected cattle enter slaughter plants during the June to September period than during the rest of the calendar year. These differences are based on survey data collected in the United States and have been independently verified by data collected in Canada.

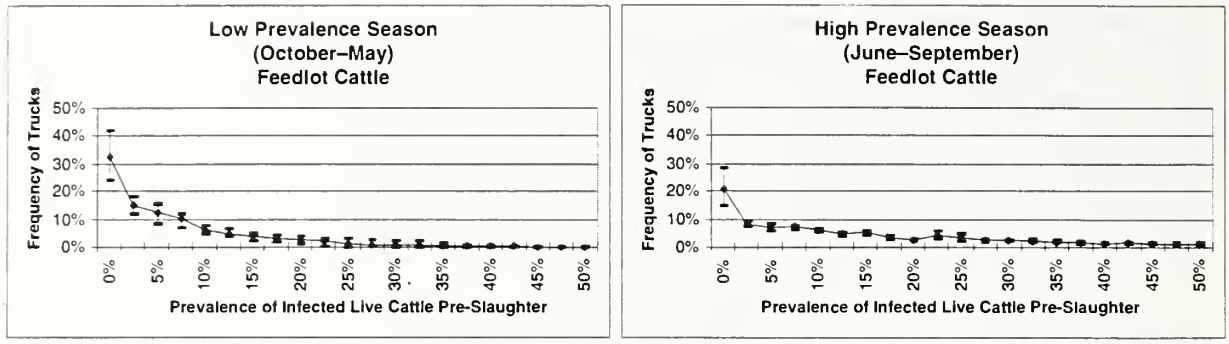

FIGURE 3-15 Comparison of seasonal distributions for prevalence of infected cattle within truckloads of feedlot cattle sent to slaughter. Error bars show the 5th and 95th percentiles of uncertainty about frequency of trucks at each prevalence level.

SLAUGHTER MODULE

The slaughter module estimates the occurrence and extent of *E. coli* O157:H7 contamination as live cattle transition to carcasses, then to meat trim, and finally to aggregates of meat trim in 60-pound trim boxes or 2,000-pound combo bins destined for commercial ground beef production. This module links the production of live cattle to the preparation of ground beef meals by consumers.

Explanation of Scope

Two types of slaughter plants are modeled: those that handle culled breeding cattle and those that handle feedlot cattle. Nevertheless, the same physical plant might slaughter both classes of cattle.

Table 3-10 shows annual slaughter numbers by plant capacity. Forty percent of culled breeding (cow/bull) cattle are slaughtered in large facilities that handle more than 1,000 head per day, while greater than 90% of feedlot (steer/heifer) cattle are slaughtered in such facilities.

TABLE 3-10 Number of Cattle Slaughtered by Type and Plant Capacity, United States, 1997

	Annual Number Slaughtered	
Plant Capacity	Breeding Cattle (Cow/Bull)	Feedlot Cattle (Steer/Heifer)
<1,000 head per day	4.4 million	2.4 million
≥1,000 head per day	3 million	26 million

Source: FSIS 1998.

The model only considers the commercial slaughter and processing of cattle. Although custom slaughter is not explicitly considered in this model, it is assumed to represent a small fraction of ground beef consumed in the United States.

Prevalence distributions of *E. coli* O157:H7 in breeding and feedlot cattle, developed in the production module, serve as inputs to the slaughter module. These distributions provide the number of infected cattle entering a slaughter plant.

Slaughter module outputs are distributions of *E. coli* O157:H7 contamination in combo bins and trim boxes. Breeder and feedlot cattle slaughtering operations are modeled separately, as are

high (June to September) and low (October to May) prevalence seasons. These distributions are inputs to the preparation module, where grinding operations begin the process of converting meat trim in combo bins or boxes into ground beef.

Definition of Key Terms

The following key terms are used throughout this module:

- Carcass refers to an animal that has been killed and had its hide removed.
- Contamination is the presence of *E. coli* O157:H7 on carcass surfaces.
- Trim is a by-product of processing carcasses to create cuts of meat (e.g., steaks, roasts) when the carcasses originate from feedlot cattle. Trim is a primary product that results from deboning carcasses that originate from breeding cattle. Trim consists of both muscle and fat.
- Combo bins are containers that hold 2,000 pounds of meat trim (Gill and Badoni 1997; Biela 1998). The containers are usually cardboard boxes lined with plastic. Many cattle may contribute meat trim to a single combo bin.
- Boxes of meat trim are similar to combo bins but only contain 60 pounds of product.
- Lot is defined as the total number of cattle necessary to fill one combo bin. A single lot may comprise one or more truckloads of cattle.

Slaughter Module Segments

The slaughter module includes seven steps: (1) arrival of live cattle at slaughter plant, (2) dehiding, (3) decontamination following dehiding, (4) evisceration, (5) final washing, (6) chilling, and (7) carcass fabrication (i.e., creation of trim) (Figure 3-16). Although there are other steps that are normally part of the slaughter process (e.g., stunning, carcass splitting), these are not explicitly modeled. Generally, these other steps are incorporated into the seven steps of the model.

Slaughterhouse operating procedures can either facilitate or mitigate the probability of *E. coli* O157:H7 contamination on beef carcasses or trim (Galland 1997). Decontamination steps can significantly reduce the numbers of *E. coli* O157:H7 and other pathogens on the carcass (Bacon et al. 1999). The model assumes that either contamination or decontamination can occur at each step of the process, with the prevalence and extent of contamination increasing if further contamination occurs and decreasing if decontamination occurs. It is possible that a decontamination process is completely effective in eliminating *E. coli* O157:H7 from a carcass, thereby reducing the prevalence of contaminated carcasses. The probability and extent of *E. coli* O157:H7 contamination or decontamination during slaughter are modeled as dependent on status of the incoming animal, type of processing plant, type of equipment and procedures used, efficacy of decontamination procedures, and sanitation processes.

Cattle arrive at slaughter plants (Step 1) via truckloads with variable prevalence of infected cattle. Because slaughter lots may consist of multiple truckloads, each truck's prevalence is estimated in this step, and the total number of infected cattle in the lot is estimated based on the total number of infected cattle on trucks contributing to a combo bin.

Dehiding (Step 2) is the transition from live cattle to carcasses. The process of removing the hide creates the first opportunity for surface contamination of the carcass with *E. coli* O157:H7 and other pathogenic and nonpathogenic microbes. The number of *E. coli* O157:H7 organisms that initially contaminate a carcass depends on the level of infected cattle, the average

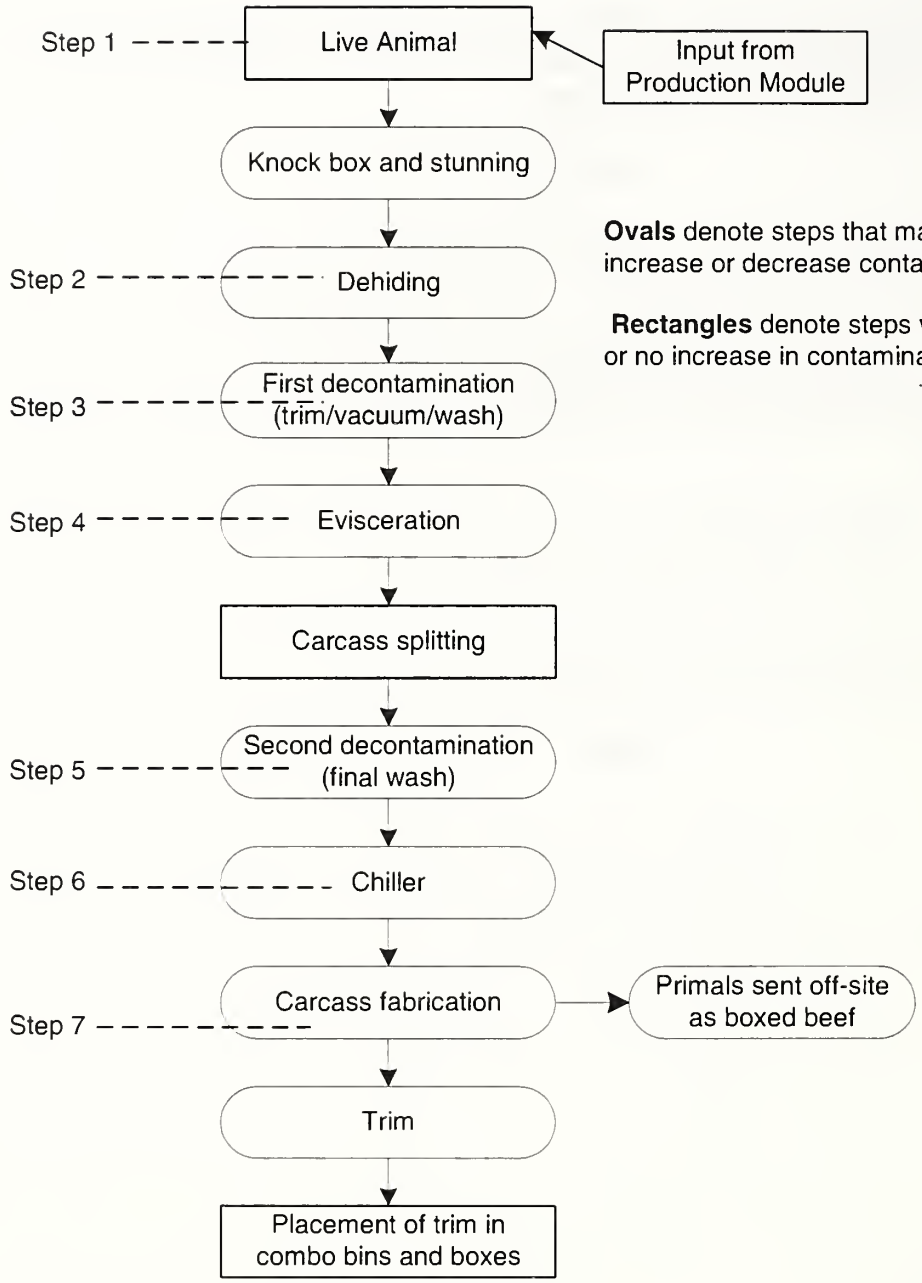

FIGURE 3-16 Steps modeled in the slaughter module.

concentration of *E. coli* O157:H7 per contaminated area, and the total area of a carcass that is contaminated (Galland 1997). Contamination introduced during dehiding can be reduced during decontamination (Step 3). During decontamination, trimming, vacuuming, or washing of the carcass surface can reduce the number of organisms on contaminated carcass surfaces (Prasai et al. 1995).

Evisceration (Step 4) is another opportunity for contamination to be introduced. If any part of the gastrointestinal tract is perforated during the evisceration procedure, *E. coli* O157:H7 contamination of muscle tissue can occur. Carcass splitting and final washing (Step 5) follow evisceration. During final washing, carcasses are washed or steam pasteurized. Washing is the

forceful application of hot or cold water to the surface of the carcass, and pasteurization is the application of steam to the surface of the carcass.

Following final washing, the carcasses move to the chiller (Step 6), where *E. coli* contamination may again increase or decrease. After chilling, the carcasses are fabricated (Step 7). Fabrication involves separating the carcass further into smaller units, trimming these units of excess fat, and—in the case of carcasses from breeding cattle—manually and/or mechanically separating muscle from bone. Feedlot carcasses are typically separated into primal (e.g., quarters) and subprimal units that are used to produce whole-muscle cuts of beef. A by-product of fabricating carcasses from feedlot cattle is meat trim, a product that is mixed and ground to produce ground beef. Because carcasses from breeding cattle produce less valuable whole muscle cuts, greater proportions of these deboned carcasses than carcasses from feedlot cattle contribute to ground beef. The boneless meat trim from one animal is distributed based on fat content into multiple combo bins or boxes, where it is mixed with trim from other cattle. Fabrication can also result in new or additional contamination through cross-contamination of work surfaces.

The following sections describe data and analysis of each slaughter step.

Modeling the Slaughter Process

Arrival of Live Animals (Step 1)

Live cattle are shipped to slaughter via trucks, where they are placed in holding pens prior to entering the knock box. The production module predicts the prevalence of infected cattle per truckload. As mentioned previously, prevalence varies by class of cattle and season. It is assumed that animals arriving at the plant together are processed together.

Number of Trucks Per Lot

The number of trucks that contribute to a slaughter lot depends on the class of cattle, the weight of trim generated per carcass, and the number of combo bins to which carcasses can contribute.

In 1998, 16.2 million steers, 10.6 million heifers, 5.9 million cows, and 0.6 million bulls were commercially slaughtered. Average carcass weights (ACW) for steers, heifers, cows, and bulls were assumed to be 764, 703, 539, and 851 pounds, respectively (NASS 1998). The proportion of carcass weight that amounts to trim (ρ) is 18% for steer/heifer carcasses, 53% for cow carcasses, and 90% for bull carcasses (Duewer 1998; AMIF 1996). These values represent midpoints of uncertainty distributions. Generally, these distributions can range $\pm$ 20%.

Trim from one steer/heifer may go into a variable number of combo bins. The actual number of bins is a function of the number of trim lines operating simultaneously in a particular plant. In steer/heifer slaughter plants, it was assumed that the number of combo bins to which an individual carcass contributes (n) ranged from 2 to 6. In cow/bull plants, this range was 2 to 4. Uncertainty about the most likely number of combo bins per carcass was modeled as a uniform(2,5) and uniform(2,3) for steer/heifer and cow/bull plants, respectively. The ranges and most likely values were modeled using triangular(min, most likely, max) distributions.

The weight of trim a carcass contributes to a single combo bin (ζ) is calculated as follows:

$$\zeta = \frac{\text{ACW} \times \rho}{n} \tag{3.8}$$

The number of carcasses per combo bin equals 2,000 pounds $\div \zeta$. It is assumed that there are 40 cattle per truckload. Therefore, this number of carcasses determines the number of truckloads

of live cattle that contribute to a combo bin (TLD). Consequently, the number of truckloads per lot is as follows:

$$\mathrm{TLD} = \frac{2000}{\zeta \times 40} \tag{3.9}$$

Number of Infected Cattle Per Truck and Lot

Number of infected cattle per truckload originating from breeding herds or feedlots has been previously calculated (Equations 3.6 and 3.7). Trucks in a lot are assumed independent. The total infected cattle in a lot (κ) is the sum of infected cattle from each truck in the lot.

Knock Box and Stunning (Not Modeled)

When it is time for slaughter, the animal is directed out of the holding pen or taken off the truck via a chute to the "knock box," where it is stunned. As the stunned animal falls, it is shackled on one hind leg, raised, and attached by a chain to an overhead rail. A knife is used to slit the throat, and the animal is bled out prior to entering the main floor of the slaughter plant.

Cross-contamination of hides is possible as cattle fall to the floor or come into contact with sides of the chute after previously *E. coli* O157:H7-contaminated cattle have passed through. Additional contamination can occur if cattle emit feces or rumen contents at the knock box (Delazari et al. 1998a, 1998b) or if dirty knives are used (Labadie et al. 1977).

The production module notes the limited data regarding prevalence of *E. coli* O157:H7 on hides and the incomplete analysis of hide sampling method sensitivity. Furthermore, the strongest correlate with carcass contamination is believed to be the fecal status of incoming cattle (Elder et al. 2000). Therefore, the stunning step is not explicitly included in the model. Nevertheless, the contribution of hide contamination to carcass contamination is implicit in the conversion of live cattle prevalence to carcass prevalence within lots.

Dehiding (Step 2)

At this step, cattle enter the main floor of the slaughter plant. Horns and hocks are removed using hydraulic cutters. The udder is removed, the head is skinned, and the hide is cut down the midline, legs, and front shanks.

Contamination Occurrence during Dehiding

The dehiding operation is where a carcass is created. It is at this point that normally sterile muscle and fat tissues on the carcass surface are exposed to microbial contaminants. An individual carcass may be self- or cross-contaminated. If the carcass originates from an animal that is not infected, contamination may occur via aerosol diffusion or contact with contaminated equipment or a contaminated carcass. If the carcass originates from an infected animal, it may be self-contaminated via fecal or hide sources or cross-contaminated by the pathways described for noninfected animals.

The exterior surface of the hide and the environment in the dehiding area are recognized sources of pathogens (Grau 1987). If any cattle are contaminated with *E. coli* O157:H7, cross-contamination can occur via workers' gloves, knives, clothing, or during the changing of the hide-puller from one carcass to the next (Gill 1999). It has been suggested that gross microbial contamination of the carcass is the result of contamination with feces from the hide, hair, hooves and ruptured gut (Siragusa et al. 1998). This contamination can occur as the hide is removed

from the carcass at several steps. For instance, the tail can flip around and create aerosols (Getz 1999) or flip back on the carcass during hide removal. Aerosol contamination can also occur when the hide separates from the carcass (Galland 1997). Hide-removing machinery called up-pullers are possibly more likely to cause aerosol contamination because the hide is being rolled up over the carcass rather than below it.

A transformation ratio (TR) relates the frequency of contaminated carcasses to the frequency of infected cattle in a lot. To estimate the fraction of carcasses contaminated during dehiding, evidence from a study in four slaughter plants is used (Elder et al. 2000). In this study, cattle fecal prevalence and carcass prevalence were measured during July and August 1999. In lots showing evidence of *E. coli* O157:H7 in cattle or on carcasses, 91 of 307 cattle (30%) and 148 of 312 carcasses at dehiding (47%) were *E. coli* O157:H7-positive. Therefore, a higher frequency of contaminated carcasses than infected cattle was detected in this study. Very sensitive testing methods were used in this study, and the results are assumed indicative of the relationship between live cattle and carcass prevalence. However, this study was completed during the summer months, and inferences drawn from it are most applicable to the high prevalence season (June to September).

It is possible that proportionally fewer carcasses are contaminated during the low prevalence season (October to May). Incoming prevalence of infected cattle is generally lower in this season. Consequently, the probability of a carcass becoming contaminated may be reduced because less contamination enters the slaughter plant environment. In a study of 12 slaughter plants conducted in September and October 1999, the prevalence of *E. coli* O157:H7 hide-contaminated cattle was 3.56%, while the *E. coli* O157:H7 prevalence of contaminated carcasses was 0.44% (Bacon et al. 2000). These results suggest a lower frequency of contaminated carcasses than contaminated cattle entering slaughter plants.

During the high prevalence season, TR is estimated from the Elder et al. (2000) data. Uncertainty about TR is modeled by incorporating these data into beta distributions (i.e., $TR = \frac{\text{beta}(148 + 1{,}312 - 148 + 1)}{\text{beta}(91 + 1{,}307 - 91 + 1)}$). Using the average TR for the high prevalence season, the frequency of contaminated carcasses is estimated to be 160% of the prevalence of incoming infected cattle.

During the low prevalence season, TR is modeled as a mixture of the beta distributions based on the Elder et al. (2000) data and a uniform distribution with a minimum approaching 0 and a maximum of the summer TR. Therefore, more uncertainty is modeled about TR during this season. Using the average TR for the low prevalence season, the frequency of contaminated carcasses is estimated to be 120% of the prevalence of incoming infected cattle.

The number of contaminated carcasses per lot (C_d) depends on the number of infected cattle per lot (κ) and TR:

$$C_d = \kappa \times \text{TR} \tag{3.10}$$

It is assumed that C_d is a random Poisson variable (i.e., $C_d \sim \text{Poisson}[\kappa \times T]$).

Level of Contamination Per Carcass

The number of *E. coli* O157:H7 organisms on a contaminated carcass at dehiding is calculated from the estimated density per cm^2 and the total contaminated surface area.

No studies have reported the density of *E. coli* O157:H7 contamination at the dehiding step. Bell (1997) measured densities of generic *E. coli* on carcasses and found 2 logs CFU/cm^2 contamination if the carcass came into contact with feces or a contaminated hide, and 1 log

CFU/cm^2 contamination due to cross-contamination (e.g., aerosols, hands, equipment, or contact with a contaminated carcass).

More relevant data regarding *E. coli* O157:H7 density on carcasses are available from the FSIS (1994) national baseline survey of slaughter plants. In this survey, a 60-cm^2 surface area was sampled from each of 2,081 chilled carcasses originating from feedlots. Four (0.2%) carcasses were *E. coli* O157:H7-positive, and enumerated densities were reported (Table 3-11).

TABLE 3-11 Enumeration of *E. coli* O157:H7 Densities on Positive Carcasses Detected by FSIS USDA (1994)

CFU/cm^2	Number of Samples	Percent of Total
<0.030	2	50
0.030 to 0.300	0	0
0.301 to 3.000	2	50
Total	4	100

Elder et al. (2000) found 6 (2%) of 330 chilled carcasses positive for *E. coli* O157:H7 using very sensitive test methods. This prevalence is substantially greater than that found in the FSIS survey (0.2%) and suggests that some contaminated carcasses were not detected in the latter survey. A ratio of these results (i.e., 0.2% ÷ 2%) suggests that about 10% of contaminated carcasses were detected in the FSIS survey and that about 90% of contaminated carcasses were below the limit of detection for that survey. This ratio (S) is modeled as follows:

$$S = \frac{\text{beta}(4+1, 2081-4+1)}{\text{beta}(6+1, 330-6+1)} \tag{3.11}$$

Additionally, of the four carcasses reported *E. coli* O157:H7-positive in the FSIS (1994) survey, two (50%) of the positive samples had densities below the measurable limit of 0.03 CFU/cm^2. Consequently, an average of about 5% of all contaminated carcasses would be expected to have values above 0.03 CFU/cm^2.

The proportion of carcasses contaminated below the measurable limit (L) is modeled as $L = S + (1 - S) \times [2 \div (4 + 1)]$. In other words, the proportion of carcasses below the measurable limit includes those carcasses not detected and those detected carcasses with unmeasurable densities. A value of one is added to the total enumerated carcasses to adjust for bias (Vose 1996).

The initial number of *E. coli* O157:H7 organisms on contaminated carcasses introduced during dehiding (I) is modeled as a cumulative frequency distribution (Table 3-12). The minimum number of *E. coli* O157:H7 organisms predicted from this distribution is 1 organism on the total contaminated surface area. The maximum number of *E. coli* O157:H7 organisms is assumed to be 3 *E. coli* O157:H7 per cm^2. Although the amount of contamination is variable, there is also uncertainty about S and the number of *E. coli* O157:H7 organisms observed in the FSIS survey (1994).

TABLE 3-12 Inputs Used to Model the Number of *E. coli* O157:H7 Organisms per Contaminated Carcass

O157 Organisms per cm^2	Cumulative Frequency (%)
0.03	$L = S + (1 - S) \times [2 \div (4 + 1)]$
Uniform(0.3,3.0)	$L + (1 - S) \times [2 \div (4 + 1)]$

There is no evidence regarding the total contaminated surface area (A) on carcasses. The total outside surface area (TSA) of steer/heifer, cow, and bull carcasses is about 32,000, 23,000, and 37,000 cm^2, respectively (McAloon 1999). Arbitrarily, the minimum area that contamination might be spread across is assumed to be 30 cm^2 (based on the measurable detection threshold). Hypothetically, the maximum area that contamination might be spread across for each carcass type is the total outside surface area. Nevertheless, initial model runs showed that contaminated surface areas greater than 3,000 cm^2 produced results that were infeasible in comparison with FSIS ground beef sampling data (see Appendix A). Therefore, uncertainty about the total contaminated surface area is modeled as $A = 10^{\text{triangular[log10(30),log(300),log(3000)]}}$.

The total number of organisms on a contaminated carcass at dehiding (OCC_d) is calculated as follows:

$$OCC_d = I \times A \tag{3.12}$$

Therefore, the maximum number of organisms on a contaminated carcass predicted by this model is 3 organisms/$cm^2 \times$ 3,000 cm^2, or 9,000 *E. coli* O157:H7 organisms, and the minimum is 1 *E. coli* O157:H7 organism per contaminated carcass.

First Decontamination (Step 3)

Following removal of the hide, one or more decontamination steps may be applied depending on the amount of visible foreign matter on the carcass. Knife trimming is used to remove visible spots of fecal contamination greater than 1 inch in diameter. Spot steam vacuuming is used to remove visible spots of fecal contamination that are less than 1 inch in diameter (FSIS 1996). Increasingly, plants are rinsing carcasses with hot water and a variety of organic acids prior to evisceration.

Any one of the three decontamination steps can reduce existing *E. coli* O157:H7 on the carcass (Bacon et al. 1999; Galland 1997). The effectiveness of knife trimming is highly variable (Prasai et al. 1995), and cross-contamination through the knife cuts can occur if inadequate knife sterilization methods are used. Sheridan et al. (1992) and Smeltzer et al. (1998) have identified equipment such as knives, gloves, and aprons as reservoirs of bacteria in the slaughterhouse.

Two experimental studies have measured the reduction of *E. coli* on inoculated beef resulting from rinsing ingesta and manure from the carcass. Gill (1999) reported that carcass rinses reduced generic *E. coli* counts by 0.32 log CFU/cm^2. Dorsa et al. (1997) reported a 0.7 log CFU/cm^2 reduction with a water rinse.

For decontamination to be effective, the procedure needs to be applied to the affected area. While visible signs of foreign matter can be readily identified and removed, bacterial colonies themselves are not directly observable. Thus, there is variability associated with the decontamination step actually encountering bacterial colonies as well as variability in any reductions in contamination. To capture this variation, the reduction from decontamination (D1) was modeled using a triangular distribution with a minimum value of 0 logs, an uncertain most

likely value ranging from 0.3 to 0.7 logs, and an uncertain maximum value ranging from 0.8 logs to 1.2 logs.

Evisceration (Step 4)

During evisceration, the ventral midline of the carcass is split and the gastrointestinal tract is removed. The remaining organs (bladder, lungs, heart, etc.) are also removed from the carcass in this stage.

Studies indicate that evisceration is usually carried out with minimal contamination (Bell 1997; Gill et al. 1996a; Gill et al. 1996b). Nevertheless, it was assumed that *E. coli* O157:H7 contamination of muscle tissue could occur if any part of the gastrointestinal tract was perforated during the sawing of the brisket (i.e., chest) and other procedures. In addition, the gastrointestinal tract of some animals may be weaker and easily tear during evisceration (Galland 1997).

Brewer (1999) suggests that perforation along the gastrointestinal tract potentially occurs in 1 out of every 100 carcasses. The probability of this event (ε) is independent of the *E. coli* O157:H7 status of the animal from which the carcass originates. Uncertainty about this probability uniformly ranges from 0% to 2%.

If the intestine of a non-*E. coli* O157:H7-infected animal ruptures during evisceration, then self-contamination of that carcass is assumed not to occur. The number of carcasses that are contaminated at evisceration (C_e) is calculated as follows:

$$C_e = \kappa \times \varepsilon \tag{3.13}$$

It is assumed that C_e is a binomial distribution (i.e., $C_e \sim$ binomial(κ, ε). If a rupture occurs in a carcass from an infected animal, then the number of *E. coli* O157:H7 that contaminate this carcass is predicted as described for dehiding ($OCC_e = I \times A$).

Carcass Splitting (Not Modeled)

At this step, the carcass is sawed in half, the tail is removed, and excess fat is trimmed away from each side. Hypothetically, the carcass might become contaminated with *E. coli* O157:H7 if a clean carcass comes into contact with contaminated machinery, hands, or other contaminated carcasses during splitting. No data are available on this type of contamination.

Second Decontamination (Step 5)

The second decontamination step occurs after carcass splitting. Different procedures for this decontamination step are used depending on the size of the plant.

Knife trimming of visibly contaminated meat occurs in both large and small plants after the carcass is split. Spot steam vacuuming may also be used in some plants. Many plants have implemented at least two decontamination interventions, such as steam pasteurization and carcass rinses, that are effective in reducing pathogens on carcasses (*Federal Register* 1998). Decontamination of carcasses can occur as visible fecal or ingesta spots are removed from the carcass via knife and/or steam vacuuming. During the carcass rinse step, *E. coli* O157:H7 can be reduced or redistributed over the entire carcass (Bell 1997). Steam pasteurization of carcasses can significantly reduce contamination, if properly done (Gill 1998).

It was assumed that large plants typically use a steam pasteurization process with four steps: (1) four sides of beef are enclosed in a stainless steel pressure chamber, (2) vertical blowers remove excess surface water, (3) steam is applied for 5 to 15 seconds, and (4) a cold water rinse

is applied. The effectiveness of this equipment depends on the temperature of the steam and the duration it is applied.

It was assumed that small plants typically use a hot water rinse, sometimes supplemented with organic acids. The effectiveness of hot water rinsing is assumed equivalent to that described for decontamination Step 1 (D1).

Efficacy of steam pasteurization has been assessed. Phebus et al. (1997) found a 3.53 ± 0.49 log CFU/cm^2 reduction in *E. coli* O157:H7 on inoculated carcasses. Gill (1998) reported up to a 2 log CFU/cm^2 reduction for generic *E. coli* from pasteurizing at 105.0°C (221.0°F) for 6.5 seconds. Nevertheless, if the carcass was not clean and dry before steam pasteurization, there was little effect from steam pasteurization. Other studies have shown reductions in prevalence of *E. coli* O157:H7-contaminated carcasses from steam pasteurization (Nutsch et al. 1997, 1998).

Kastner (1998) reported that steam pasteurization was effective in reducing *E. coli* O157:H7 only if the temperature was 93.3°C (200.0°F) for 6 seconds or more. Phebus (personal communication 1999) suggested that the standard industry practice uses 87.8°C (190.0°F) steam for 6 to 8 seconds.

Given standard industry behavior and available evidence, variability in steam pasteurization efficacy (i.e., D2 for large plants) was modeled using a triangular distribution with a minimum value of 0 logs, an uncertain most likely value of 0.5 to 1.5 logs, and an uncertain maximum value of 1.51 to 2.5 logs.

Chiller (Step 6)

After the sides of beef are decontaminated for the second time, they go into a blast air chiller for 24 to 48 hours. FSIS regulations require chilling deep muscle (6 inches) to 10.0°C (50.0°F) within 24 hours and to 7.2°C (45.0°F) within 36 hours (NACMCF 1993). Sides of beef are automatically or manually spaced on overhead rails within the chiller and are periodically sprayed with water. Occasionally distilled water, chlorine, or a lactic acid solution may also be used. After chilling, the sides are unloaded, graded, and sorted.

Growth or decline of *E. coli* O157:H7 on the surface of carcasses is largely a function of time and temperature. Fluctuations in chiller temperature, or the outright failure to adequately chill carcasses, may enable growth. Gill and Bryant (1997) reported that generic *E. coli* counts increased by 0.25 logs in one slaughterhouse and decreased by 1.34 log CFU/cm^2 in another slaughterhouse. Dorsa (1997) found a 1.2 log CFU/cm^2 increase in *E. coli* O157:H7 on carcasses stored for 2 days in the chiller at 5.0°C (41.0°F). Although deep tissue mass cools slowly, it is generally sterile and thus not necessarily a problem (Bailey and Cox 1976; Gill 1979).

Growth or decline is assumed only to occur on carcasses where *E. coli* O157:H7 is already present before entering the chiller. Changes to *E. coli* O157:H7 populations on carcasses during chilling (CH) are modeled using a normal distribution with an uncertain mean ranging from –0.5 to 0.5 logs and a standard deviation of 1 log. Therefore, the most likely effect from chilling is that there is no change in the *E. coli* O157:H7 count on carcasses, yet substantial changes can occur with nonnegligible frequency (e.g., 2 or more logs of growth can occur in 2.5% of lots).

Carcass Fabrication (Step 7)

Carcasses move from the chiller to the fabrication floor, which is usually maintained at 10°C (50°F). The fabrication step is complicated and typically involves many plant personnel operating on different lines to process different parts of the carcass.

In feedlot cattle plants, sides of beef enter the fabrication step on overhead rails where they are cut into primals (major cuts of beef) and subprimals (minor cuts of beef). Most primal cuts

are taken from the rail using a hook and knife. Leftover trim moves on conveyers to either the combo bins or to a vacuum packaging area. The trim is either put into combo bins to which dry ice is added prior to shipment, or it is vacuum packaged and put into boxes maintained at a temperature between 0°C and 2°C (32.0°F to 35.6°F).

The fabrication area in slaughter plants is cleaned at the end of each day with a hot water power washer that may contain sanitizers. Larger pieces of meat and trim are periodically picked off equipment and carted away. Knives, chain-mail aprons, and gloves are washed with hot water.

During the cutting and deboning operations, contamination is possible from environmental sources and contaminated sides of beef. The major source of contamination is likely to be the surface of incoming carcasses. Freshly cut surfaces of meat may be further contaminated when in contact with processing surfaces, equipment, conveyer belts, cutting surfaces, knives, gloves, and aprons during slaughter (Charlebois et al. 1991). Gill et al. (1999) found that despite a stringent sanitation regimen, and inspection by the national regulatory authority and internal plant quality assurance staff, *E. coli* O157:H7 persisted and proliferated on conveyer equipment in obscure areas that continued to contaminate the meat-contacting surface.[1]

Cross-contamination can occur via workers' hands and the commingling of trim (Newton et al. 1978). Fabrication rooms are typically kept at 10°C (50°F), but lapses may occur and the higher temperatures that result enable microbial growth. Gill (1996) has demonstrated that the practice of cooling meat trim with dry ice in combo bins is generally effective in preventing *E. coli* O157:H7 growth. Scanga et al. (2000) found no difference in the concentration of *E. coli* O157:H7 across fat content. Prasai et al. (1995) found no difference in concentrations of *E. coli* O157:H7 between hot deboning and cold deboning.

Minimal data are available on frequency and amounts of *E. coli* O157:H7 contamination during the fabrication process. Three studies report increases in general bacterial growth during this process. Hardin et al. (1995) report increased bacterial contamination on beef surfaces during the trimming process even with the use of sterile utensils under experimental conditions. Charlebois et al. (1991) sampled four locations within fabrication and concluded that the deboning operations resulted in the highest final count of fecal coliforms on boneless beef. Specifically, it was found that of 378 samples, the percent of samples that had more than 500 fecal coliform/cm^2 increased from 0.8% to 6.6%. A study in four plants found increases in generic *E. coli* contamination during fabrication ranging from 0 to 2 logs CFU/cm^2 (Gill 1999).

The data suggest that the fabrication step might result in increased *E. coli* O157:H7 populations on meat trim. The quantitative evidence is limited. Therefore, the fabrication effect is indirectly estimated.

This indirect estimate results from the output of the grinder segment in the preparation module. FSIS ground beef sampling data for 2000 were used to set upper and lower limits for ground beef contamination (see Appendix A). Simulations of the slaughter segment that resulted in expected contamination greater than the upper limits were discarded as implausible. Simulations of the slaughter segment that resulted in expected contamination below the lower limits had additional contamination added. This additional contamination represents the effect of fabrication (F).

During the low prevalence season, the model estimates the average effect from fabrication to be 0.33 logs. This effect can range from 0 logs to 1.5 logs because of uncertainty in the model

[1]The cleaning regimen involved "the cleaning of the carcass breaking equipment, the removal of gross detritus by brushing and sweeping, washing with high pressure sprays of cold water, coating with a foaming detergent, washing with high pressure sprays of hot water, and treatment of the cleaned equipment with a chlorine sanitizer" (Gill et al. 1999).

inputs and methods. A 0.33 log increase implies that contamination levels entering combo bins are more than doubled (i.e., $10^{0.33} = 2.1$) as a result of fabrication. During the high prevalence season, the increase from fabrication is 0.22 logs, with a similar range of uncertainty. Therefore, the average effect of fabrication is estimated to be substantial from this model. This conclusion supports the suggestion of some researchers that fabrication is a critical step for *E. coli* O157:H7 transfer and amplification within the slaughter process.

Contamination in Combo Bins and Boxes

Contamination from a Single Carcass

For each carcass contaminated during the dehiding step (but not during evisceration), the number of *E. coli* O157:H7 organisms (E_d) after fabrication is calculated as follows:

$$E_d = (\mathrm{OCC_d} \times 10^{-DC1} \times 10^{-DC2} \times 10^{CH} \times 10^{F}) \qquad (3.14)$$

In other words, the number of organisms initially on the carcass ($\mathrm{OCC_d}$) is proportionally reduced by the log reductions predicted by $DC1$ and $DC2$, proportionally increased or decreased during the chilling step (CH), and proportionally increased during fabrication (F) (Table 3-13).

TABLE 3-13 Illustrative Example for Calculating the Number of Organisms Remaining on a Single Carcass Following Fabrication. In this scenario, contamination only occurs at dehiding. Therefore, the evisceration step is omitted in this example.

Steps	Symbol	Example Value	Comments
Dehiding (2)	$\mathrm{OCC_d}$	100 organisms	
First decontamination (3)	DC1	0.5 logs	$10^{-0.5} = 0.32$, Step 3 results in a 68% reduction in organisms.
Second decontamination (5)	DC2	1 log	$10^{-1} = 0.1$, Step 5 results in a 90% reduction in organisms.
Chilling (6)	CH	0 logs	$10^{0} = 1$, Step 6 results in no change in organisms.
Fabrication (7)	F	1 logs	$10^{1} = 10$, Step 7 results in a tenfold increase in organisms.
Organisms remaining (Equation 3.4 through 3.13)	E	32 organisms	

For a carcass contaminated only at evisceration, the number of *E. coli* O157:H7 organisms (E_e) remaining after fabrication is calculated similarly:

$$E_e = (\mathrm{OCC_e} \times 10^{-DC2} \times 10^{CH} \times 10^{F}) \qquad (3.15)$$

Because evisceration contamination occurs after the first decontamination step in the process, the first decontamination step does not influence the final number of organisms remaining on this carcass.

For a carcass contaminated at both the dehiding and evisceration steps, the number of *E. coli* O157:H7 organisms (E_f) remaining on the carcass after fabrication is calculated as follows:

$$E_f = \left[(\mathrm{OCC_d} \times 10^{-DC1}) + \mathrm{OCC_e}\right] \times 10^{-DC2} \times 10^{CH} \times 10^{F} \qquad (3.16)$$

Given any E and the surface area contaminated (A), the density of *E. coli* O157:H7 contamination (η) on a carcass is calculated as follows:

$$\eta = \frac{E}{A} \tag{3.17}$$

The amount of *E. coli* O157:H7 is signified as η_d, η_e, η_b to indicate the type of carcass contamination.

All of the *E. coli* O157:H7 contamination is assumed to be on the surface of the carcass. Seventy-five percent of a steer/heifer carcass surface area is estimated to end up in ground beef (McAloon 1999). For cow/bull carcasses, approximately 90% of the surface area goes into trim. The number of cm^2 per pound of trim (φ) depends on the total surface area, the percent of surface area that becomes trim, and the total weight of trim. It is calculated as

$$\varphi = \frac{\mathrm{TSA}_a}{\mathrm{ACW} \times \rho}, \tag{3.18}$$

where TSA_a is the total surface area adjusted for the percent trim.

For each carcass, the pounds of trim a single carcass contributes to a combo bin are previously calculated as ζ (Equation 3.8). Therefore, the total cm^2 placed into a combo bin per carcass is the product of ζ and φ.

Some fraction of the total surface area placed into a combo bin from a carcass is contaminated with *E. coli* O157:H7. This fraction depends on the total cm^2 placed in the combo bin ($\zeta \times \varphi$) and the probability of a contaminated cm^2 ($\mathrm{A} \div \mathrm{TSA}$). The number of contaminated cm^2 a carcass contributes to a combo bin (CC) is distributed as follows:

$$\mathrm{CC} \sim \mathrm{Binomial}(\zeta \times \varphi, \frac{\mathrm{A}}{\mathrm{TSA}}) \tag{3.19}$$

The total number of *E. coli* O157:H7 organisms a carcass contributes to a combo bin (CBO) depends on the number of *E. coli* O157:H7 organisms on the carcass per contaminated cm^2 and the total contaminated cm^2 entering the combo bin. It is distributed as follows:

$$\mathrm{CBO} \sim \mathrm{Poisson}(\eta \times \mathrm{CC}) \tag{3.20}$$

Contamination from Entire Lot

A combo bin consists of the contributions from many carcasses. *E. coli* O157:H7 contamination contributed to a combo bin can come from cattle that are contaminated at dehiding, or evisceration, or at both steps. The probability that a carcass is contaminated at evisceration depends on it being from an infected animal. In contrast, carcasses contaminated at dehiding may either originate from infected or noninfected cattle. The probability that a dehiding-contaminated carcass is also from an infected animal is unknown but is assumed uniform(0,1). If a lot consists of carcasses that are contaminated at dehiding and at evisceration (as predicted by C_d and C_e), then the number of carcasses contaminated at both sites (C_b) is predicted as binomial [minimum(C_d,C_e),uniform(0,1)]. Therefore, the number of carcasses contaminated only at dehiding is $C_d - C_b$, and the number of carcasses contaminated only at evisceration is $C_e - C_b$.

The amount of *E. coli* O157:H7 contamination in a combo bin depends on the number of contaminated carcasses and the amount of contamination each carcass contributes. The total

amount of *E. coli* O157:H7 contributed by dehiding-contaminated carcasses ($TCBO_d$) is calculated as follows:

$$TCBO_d = \sum_{0}^{C_d - C_b} \text{Poisson}(\eta_{d_i} \times CC_i) \quad (3.21)$$

Similarly, the total amount of *E. coli* O157:H7 contributed by eviscerator-contaminated carcasses ($TCBO_e$) and those carcasses contaminated at both steps ($TCBO_b$) are calculated as follows:

$$TCBO_e = \sum_{0}^{C_e - C_b} \text{Poisson}(\eta_{e_i} \times CC_i) \text{ and} \quad (3.22)$$

$$TCBO_b = \sum_{0}^{C_b} \text{Poisson}(\eta_{b_i} \times CC_i) \quad (3.23)$$

The total *E. coli* O157:H7 in a combo bin (TCBO), therefore, is calculated as follows:

$$TCBO = TCBO_d + TCBO_e + TCBO_b \quad (3.24)$$

Boxes

Boxes are 60-pound versions of combo bins. Therefore, the number of *E. coli* O157:H7 in a box (TBXO) is calculated as follows:

$$TBXO = \text{Poisson}\left(TCBO \times \frac{60 \text{ pounds}}{2000 \text{ pounds}}\right) \quad (3.25)$$

Slaughter Module Results

Outputs from the slaughter module are distributions describing the frequency of *E. coli* O157:H7 in combo bins (and boxes) generated during high and low prevalence seasons for cow/bull and steer/heifer slaughter plants. These outputs become inputs to the preparation module, in which the contents of combo bins (i.e., trim) are processed to produce ground beef.

Combo Bins

Figure 3-17 shows distributions of *E. coli* O157:H7 contamination in combo bins generated from the slaughter of cows and bulls. These results were estimated from 100 simulations of the model. During the low prevalence season, the mean frequency of combo bins containing no *E. coli* O157:H7 is 94%, but this frequency might range between 88% and 97% because of uncertainty in model inputs. During the high prevalence season, an average of 92% (ranging from 85% to 97%) of combo bins contain no *E. coli* O157:H7. Therefore, an average of 6% and 8% of combo bins generated from breeding cattle are contaminated with 1 or more *E. coli* O157:H7 organisms during the low and high prevalence seasons, respectively. Furthermore, the average combo bin contains 2 and 3 *E. coli* O157:H7 organisms in the low (October to May) and high (June to September) prevalence seasons, respectively.

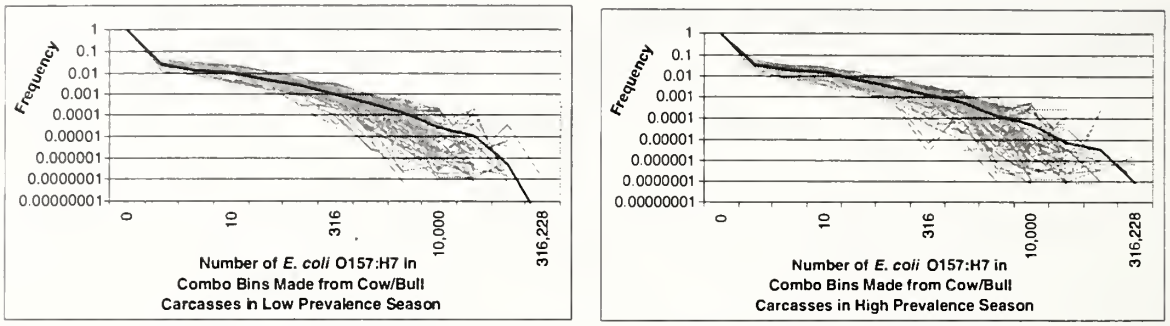

FIGURE 3-17 Comparison of seasonal distributions for number of *E. coli* O157:H7 in combo bins constructed from the slaughter of breeding (cow/bull) cattle. Dark lines are the mean distributions for each season.

Figure 3-18 shows distributions of *E. coli* O157:H7 contamination in combo bins generated from the slaughter of steers and heifers. These results were also estimated from 100 simulations of the model. During the low prevalence season, an average of 77% (ranging from 55% to 97%) of combo bins generated from steer/heifer carcasses contained no *E. coli* O157:H7. During the high prevalence season, 57% (ranging from 42% to 83%) of these combo bins contained no *E. coli* O157:H7. Therefore, an average of 23% and 43% of combo bins contain 1 or more *E. coli* O157:H7 organisms during the low and high prevalence seasons, respectively. Furthermore, the average combo bin contains 13 and 41 *E. coli* O157:H7 organisms in the low and high prevalence seasons, respectively.

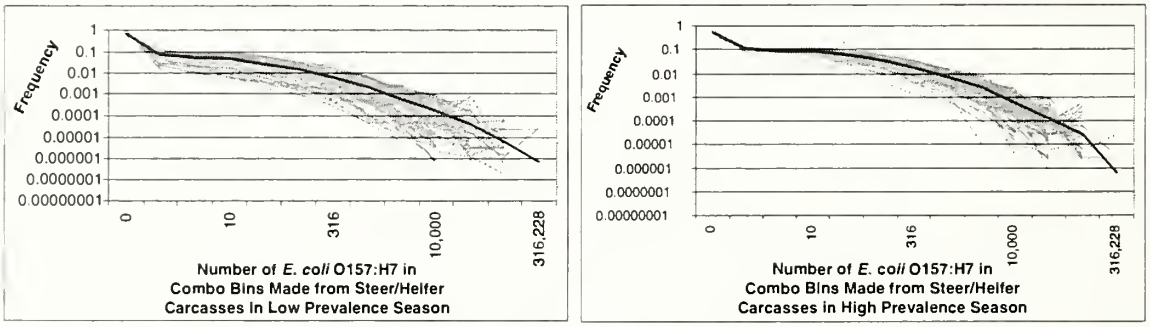

FIGURE 3-18 Comparison of seasonal distributions for number of *E. coli* O157:H7 in combo bins constructed from the slaughter of feedlot (steer/heifer) cattle. Dark lines are the mean distributions for each season.

These results show that prevalence and contamination levels in combo bins increase during the high prevalence season. These seasonal differences in combo bin contamination reflect the trends in prevalence of infected cattle entering slaughter. As noted previously, the influence of season is much greater for feedlot cattle than for breeding cattle. For combo bins generated from feedlot cattle, prevalence of contaminated combo bins increases nearly twofold, and average contamination levels increase over threefold, during the high prevalence season. Therefore, ground beef generated from steer/heifer combo bins is likely to be substantially more contaminated during the June to September period than ground beef produced during the other months of the year.

These results also show that combo bins generated from steer/heifer carcasses are more likely to be contaminated than those generated from cow/bull carcasses. On average, there is about a

fourfold greater prevalence of contaminated combo bins generated from steer/heifer carcasses compared with those generated from cow/bull carcasses during the low prevalence season. This difference is over fivefold during the high prevalence season. These differences reflect the differences noted for incoming live cattle prevalence between these two classes of cattle.

Boxes

Figure 3-19 shows distributions of *E. coli* O157:H7 contamination in meat trim boxes generated from the slaughter of cows and bulls. These results were estimated from 100 simulations of the model. During the low prevalence season, an average of 99% of boxes (ranging from 97% to 100%) contain no *E. coli* O157:H7. During the high prevalence season, an average of 98% of boxes contain no *E. coli* O157:H7. Therefore, about 1% and 2% of boxes generated from breeding cattle are contaminated with 1 or more *E. coli* O157:H7 organisms during the low and high prevalence seasons, respectively. Regardless of season, the average box concentration is much less than 1 *E. coli* O157:H7 organism in the low and high prevalence seasons.

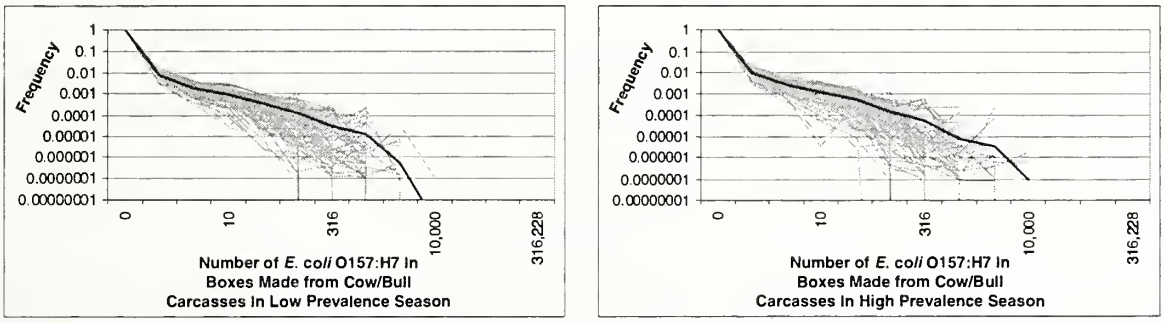

FIGURE 3-19 Comparison of seasonal distributions for number of *E. coli* O157:H7 in 60-pound boxes constructed from the slaughter of breeding (cow/bull) cattle. Dark lines are the mean distributions for each season.

Figure 3-20 shows distributions of *E. coli* O157:H7 contamination in meat trim boxes generated from the slaughter of steers and heifers. These results were also estimated from 100 simulations of the model. During the low prevalence season, an average of 94% (ranging from 87% to 99%) of boxes generated from steer/heifer carcasses contained no *E. coli* O157:H7. During the high prevalence season, 87% (ranging from 79% to 97%) of these boxes contained no *E. coli* O157:H7. Therefore, about 6% and 13% of boxes contain 1 or more *E. coli* O157:H7 during the low and high prevalence seasons, respectively. The average box contains almost 0.5 and 1 *E. coli* O157:H7 organisms in the low and high prevalence seasons, respectively.

By definition, boxes consist of less meat trim than combo bins. Consequently, prevalence and levels of *E. coli* O157:H7 in these aggregates of meat trim are less than observed for combo bins. However, the number of ground beef servings generated from boxes is correspondingly reduced. Therefore, the risk to consumers from ground beef generated from boxes is not likely to be much different from the risk from ground beef generated from combo bins. Seasonal trends and cattle class differences noted for combo bins are also noted for boxes.

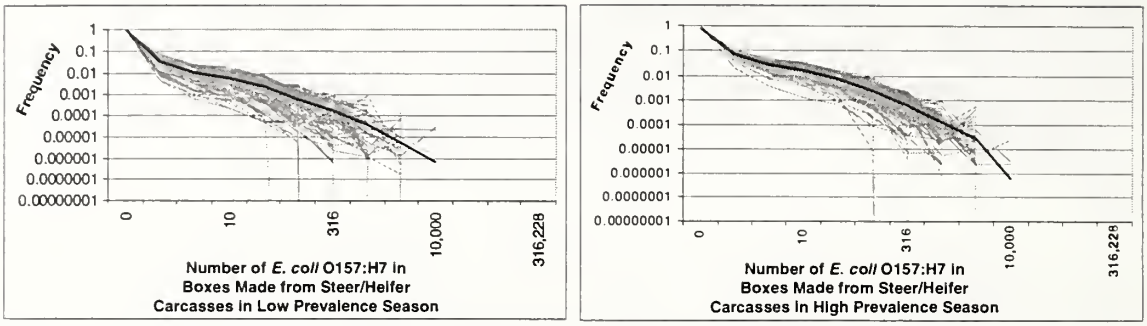

FIGURE 3-20 Comparison of seasonal distributions for number of *E. coli* O157:H7 in 60-pound boxes constructed from the slaughter of feedlot (steer/heifer) cattle. Dark lines are the mean distributions for each season.

PREPARATION MODULE

The preparation module estimates the occurrence and extent of *E. coli* O157:H7 contamination in consumed ground beef servings. This module also characterizes the consumption of ground beef servings by age of consumer and location of meal.

Explanation of Scope

The preparation module simulates the annual consumption of approximately 18 billion ground beef servings. It considers the effects of handling and cooking on the amount of *E. coli* O157:H7 in contaminated servings. Ground beef is consumed in many forms. Typical forms are hamburger patties, ground beef as a formed major ingredient (e.g., meatballs and meat loaf), and ground beef as a granulated ingredient (e.g., ground beef in spaghetti sauce). The model focuses on the first two forms. Because granulated ground beef has a relatively large surface area compared with volume, the effect of cooking on this product is considered to be similar to intact beef products. Intact beef products are considered to be safe after cooking (NACMCF 1997). Furthermore, products incorporating granulated ground beef are often subjected to further cooking. Consequently, these types of products are assumed to have no viable *E. coli* O157:H7 organisms and are not modeled.

Although cross-contamination could be a potential contributor for contamination of ground beef product, cross-contamination of ground beef products is not modeled. An analysis of potential pathways in which ground beef could be contaminated by food service workers or other foods—or alternatively, pathways in which ground beef could contaminate other products—is beyond the scope of this risk assessment. Currently, quantitative modeling of cross-contamination in foods is hampered by a dearth of evidence. Furthermore, cross-contamination pathways are potentially complex, and each pathway may require as much data regarding growth dynamics and cooking effect as the primary product of interest. The model, however, can serve as a starting point for analyzing the effects of cross-contamination on human exposure to *E. coli* O157:H7.

Definition of Key Terms

The following key terms are used throughout this module:

- Servings are defined as an "eating occasion" within the 1994–1996, 1998 Continuing Food Survey of Individual Intakes (CSFII) database. The amount of ground beef consumed per eating occasion varies by age of the consumer and location where the meal was consumed (i.e., at home versus away from home).
- Exposure refers to the amount of contamination that is consumed in a serving.
- Home is used when servings are prepared and served in a home environment.
- Away from home is used when servings are prepared and served in an institutional environment. This is often referred to as "HRI" (hotels, restaurants, and institutions).
- Transportation refers to nonrefrigerated transport of product from a retail or wholesale establishment to its place of preparation and consumption.
- Retail refers to establishments, such as grocery stores or butcher shops, that sell ground beef for home consumption.
- Wholesale refers to establishments that serve as distributors for HRI for away from home consumption.
- High prevalence season refers to June through September.
- Low prevalence season refers to October through May.

Preparation Module Segments

The preparation module consists of six primary steps (Figure 3-21). Five of these steps explicitly model growth, decline, or dispersion of *E. coli* O157:H7 contamination: (1) grinding, (2) storage during processing by the retailer or distributor, (3) transportation home or to HRI, (4) storage at home and "away from home" (i.e., HRI), and (5) cooking. Step 6 models the amount of ground beef consumed, which varies depending on the age of the consumer and the location where the meal was consumed.

Inputs to this module consist of the frequency and extent of *E. coli* O157:H7 contamination in combo bins and boxes estimated in the slaughter module. The preparation module output consists of a single exposure distribution depicting the frequency and extent of *E. coli* O157:H7 contamination consumed in a year.

Grinding (Step 1) transforms combo bins and boxes into ground beef. Combo bins are processed in large commercial facilities, and boxes are typically processed in smaller settings such as grocery stores.

In Step 1, multiple combo bins or boxes are combined, mixed, and extruded to produce finished ground beef with a specific fat content. For example, a combo bin consisting of 90% lean trim can be mixed with another combo bin of 50% lean trim to make a grinder load of 70% lean ground beef. Although the extent of *E. coli* O157:H7 contamination does not increase during the grinding process because of temperature controls, contamination from a single combo bin or box can be dispersed during grinding to contaminate many individual ground beef servings. Consequently, assuming a constant frequency of contaminated combo bins, the number of combo bins that contribute to a grinder load determines whether the grinder load is contaminated. Once ground beef is produced, it can be shaped into patties or packaged in bulk containers and shipped for eventual consumption. Some beef is also ground at retail or institutional sites. This beef consists of 60-pound boxes, in addition to trim generated in the facility and beef that has already been ground at a grinding facility.

Storage conditions at retail or wholesale (Step 2) provide an opportunity for *E. coli* O157:H7 levels to (a) increase as a result of time and temperature abuse or (b) decrease as a result of the effects of freezing ground beef (Ansay et al. 1999; Sage and Ingham 1998). Ground beef is

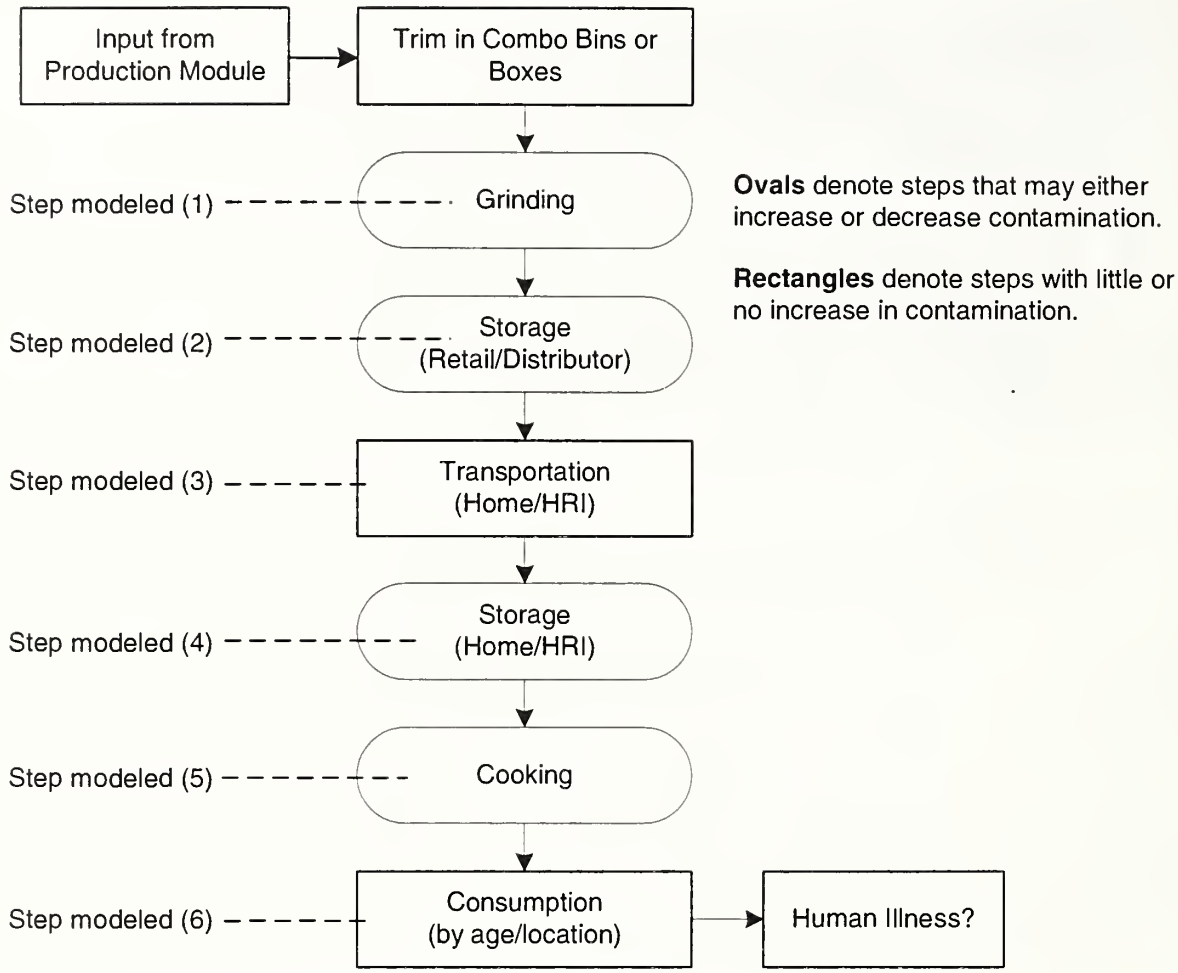

FIGURE 3-21 Steps modeled in the preparation module.

subject to a variety of temperatures during storage and handling conditions, depending on its site of production and ultimate use. These conditions at home and in HRI can significantly increase the numbers of *E. coli* O157:H7 in ground beef (Marks et al. 1998; Buchanan and Bagi 1994; Walls and Scott 1996).

Step 3 models the effects of time and temperature during transportation on the level of *E. coli* O157:H7 after the ground beef is purchased.

Step 4 models the storage of ground beef in the freezer or refrigerator prior to its preparation and consumption and provides another opportunity for increases or decreases in *E. coli* O157:H7 contamination in ground beef servings.

Ground beef is usually cooked prior to consumption (Step 5). Cooking can significantly reduce *E. coli* O157:H7 in ground beef servings (D'Sa et al. 2000; Juneja et al. 1997; Jackson et al. 1996). The model uses final internal product temperature data from a commercial food temperature database (Audits International 1999) to determine the level of reduction in *E. coli* O157:H7 contamination in ground beef servings.

Step 6 models consumption of *E. coli* O157:H7-contaminated ground beef servings, taking into consideration the age group of the consumer (i.e., 0 to 5, 6 to 24, 25 to 65, and 65+ years of age) and where the meals were consumed (i.e., at home or away from home).

The following sections describe data and analysis for each preparation step.

Modeling the Preparation Process

Input from the Slaughter Module

The slaughter module provides distributions for *E. coli* O157:H7 contamination in combo bins and boxes by season for breeding (cow/bull) and feedlot (steer/heifer) cattle slaughter plants. Combo bins can be mixed across slaughter plant type (i.e., combo bins originating from cow/bull plants can be mixed with combo bins originating from steer/heifer plants). Combo bins are characterized by the "leanness" of the ground beef. Requirements for specific fat content in ground beef dictate which combo bins are mixed.

Grinding Beef Trim (Step 1)

Ground beef produced in the United States is sold to the general public through retail establishments (41%) or to HRI through wholesale distributors (59%) (APHIS:VS:CEAH 1994). Retail establishments may use coarse ground beef and mix it with trimmings produced in-house. They may also buy "case ready chubs" (plastic tubes filled with 5 to 10 pounds of ground beef). About 22% of retail ground beef contains at least some retail trimmings (APHIS:VS:CEAH 1994). Of the ground beef used in HRI, 98% percent comes directly from grinder establishments.

E. coli O157:H7 contamination in beef trim generated in the slaughter module is used as an input to the grinding step in the preparation module. As noted in the slaughter module, beef trim is generated either from cows and bulls or from steers and heifers. Although individual cows and bulls generate more trim than individual steers and heifers, the slaughtering of greater numbers of steers and heifers results in about 60% of domestic beef trim coming from this source (Table 3-14). As noted previously, about 15% of beef is imported and either used by itself or mixed with domestic product. It is assumed that this product is similar to domestically produced product. Figure 3-22 depicts the three types of beef used to make ground beef (i.e., beef trim from cows/bulls or steers/heifers, imported beef trim, or ground beef).

TABLE 3-14 Percent of Meat Trim by Types of Cattle (Cows, Bulls, Steers, and Heifers)

Carcass Type	Average Carcass Weight (lbs.)	Percent Trim	Annual Slaughter (Million Head)	Total Meat Trim (Million lbs.)	Percent of Trim by Class
Cow	539	53%	6.9	1,970	40% Cow/Bull
Bull	851	90%	0.7	540	
Steer	764	18%	17.4	2,390	60% Steer/Heifer
Heifer	703	18%	11.2	1,420	

The model combines combo bins of three types of beef trim (Figure 3-22) to simulate a grinder load of beef. It includes beef that may be blended with other ground beef after initial grinding. For example, beef from two separate grinder loads of 10,000 pounds representing five combo bins each could be further mixed together to create a grinder load of 20,000 pounds. The number of combo bins (NCB) that are mixed together to create a grinder load ranges uniformly from 2 to 15 (Smith 1998, personal communication).

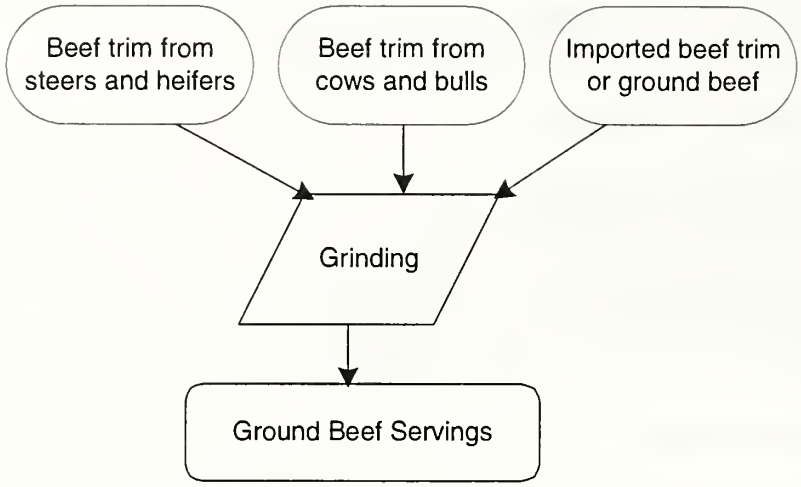

FIGURE 3-22 Inputs to grinding (Step 1).

Retail ground beef is modeled as coming from one to seven 60-pound boxes of beef trim. Equation 3.26 represents the process as modeled for combo bins:

$$\underset{\text{in grinder load}}{E.coli\ \text{O157:H7}} = \sum_{2}^{NCB} \text{Discrete}\left[\left(\begin{matrix}E.coli\ \text{O157:H7} \\ \text{in combo bin}_i\end{matrix}\right),(P_i)\right]_{\infty}^{\infty} \tag{3.26}$$

The discrete distribution in Equation 3.26 consists of two arrays. The first array represents various contamination levels that may occur in a combo bin, and the second array represents the corresponding probability of the occurrence of each *E. coli* O157:H7 contamination level.

After *E. coli* O157:H7-contaminated beef trimmings have been ground, the next load may be contaminated unless the grinder has been thoroughly cleaned and sanitized. Farrell et al. (1998) reported that ground beef inoculated with 6 logs of *E. coli* O157:H7 per gram resulted in contamination of a grinder with approximately 3 logs per cm^2. Washing the grinder lowered the contamination to about 1 log per cm^2. Sanitizing the grinder further lowered the contamination to less than 1 log per cm^2. Initial contamination of ground beef in a grinder with 2 logs of *E. coli* O157:H7 per gram followed by cleaning and sanitizing with chlorine resulted in no detection of *E. coli* O157:H7 organisms. This "carryover" *E. coli* O157:H7 contamination between grinder loads was not modeled because (1) Farrell et al. (1998) show that even without cleaning and sanitizing between grinder loads, there was still a 3 log reduction in the number of *E. coli* O157:H7 organisms; (2) the number of *E. coli* O157:H7 organisms present in grinder loads is very low and is therefore assumed not to contribute significantly to contamination of the next grinder load; and (3) such carryover contamination could potentially increase the number of contaminated grinder loads but would result in a corresponding decrease in the number of *E. coli* O157:H7 in the previous grinder load.

Storage and Transportation (Steps 2 through 4)

From the time that ground beef is produced until it is prepared and consumed, it is stored under varying conditions. Ground beef product may be produced at the slaughter establishment, shipped immediately to retail, purchased shortly thereafter, and prepared. Product could also be produced from beef trim that was sent to a grinding establishment where it was held before it was shipped to a wholesaler and stored for additional time. It could then be purchased in bulk by an HRI establishment and stored in a freezer before refrigeration, thawing, and final preparation.

In addition to variations in storage time, variations in fat content of the ground beef, strain of *E. coli* O157:H7, and packaging can also contribute to growth or decline in the number of *E. coli* O157:H7 organisms in ground beef.

Modeling Growth

Increase or decrease in the number of *E. coli* O157:H7 organisms in ground beef is based on the time in which ground beef is stored at certain temperatures. This risk assessment models growth of *E. coli* O157:H7 in ground beef based on three assumptions:

1. All areas of a product are at the same temperature. In reality, the outside of the product would reach a stable temperature first, with the inside of the product reaching a stable temperature last. To construct corresponding cooling curves, however, would require data and assumptions about the frequency of product thickness, its correlation to storage temperature, and the corresponding times of storage. The result would be a much more complicated model that would not be more useful because the underlying assumptions would not be well supported.
2. All *E. coli* O157:H7 strains exhibit the same growth characteristics in any ground beef product. This risk assessment model further assumes that temperature during storage and handling is the only significant variable to predict growth. Although factors other than temperature are known to influence the growth of *E. coli* O157:H7 (Buchanan and Bagi 1994), this simplifying assumption is necessary to permit modeling. Nevertheless, variability in growth is modeled based on the available evidence.
3. Lag period duration in any one stage is affected by temperatures in previous stages. The lag period (the time prior to cell division) duration is modeled as a cumulative percentage that begins at 100% and decreases as product is subjected to varying temperatures at different stages along the farm-to-table continuum. Although it is reasonable to assume that *E. coli* O157:H7 organisms exposed to significantly different storage conditions would need additional time to adjust to those conditions before entering into a rapid growth phase, this assumption avoids the complications of making additional assumptions about when to restart calculations for lag period duration. As a result, this assumption in the risk assessment may result in an overestimation of the increase in the number of *E. coli* O157:H7 organisms in ground beef during storage and handling.

Estimation of the effect of storage temperatures on the growth and decline of *E. coli* O157:H7 is based on two types of data:

- consumer and retail time and temperature data from commercial food temperature databases (Audits International 1999), and
- predictive microbial growth data for *E. coli* O157:H7 in ground beef from published scientific literature (Ansay et al. 1999; Marks et al. 1998; Sage and Ingham 1998; Jackson et al. 1996; Walls and Scott 1996; Buchanan and Bagi 1994).

Several studies show the effect of temperature on *E. coli* O157:H7 levels in ground beef. Palumbo (1997) reported that *E. coli* O157:H7 grows at 8°C (46.4°F) but not at 5°C (41°F). Gill and Bryant (1997) reported a decline of generic *E. coli* as a result of freezing. Ansay et al. (1999) tested the effects of refrigeration over time. In this study, storage of ground beef patties at 2°C for 4 weeks resulted in a 1.9 log reduction of *E. coli* O157:H7, and storage at –2°C for 4 weeks resulted in a 1.5 log reduction. Freezing (–20°C) for 1 year resulted in a 1 to 2 log reduction while tempering (at 15°C for 4 hours) increased the log reduction brought about by storage at –2°C. Sage and Ingham (1998) tested the effects of freezing (–20°C, 24 hours) and thawing on *E. coli* O157:H7 in ground beef and found a wide range in freeze-thaw sensitivity, with a decrease in *E. coli* O157:H7 levels from 0.62 to 2.52 logs per gram.

Predictive microbiological models have been developed for *E. coli* O157:H7 in ground beef under various storage conditions. These microbiological models predict the growth and decline of *E. coli* O157:H7 given environmental parameters including time, temperature, pH, and salinity. One set of equations was developed by Buchanan and Bagi (1994) and was later incorporated into the Pathogen Modeling Program (PMP) available from the Agricultural Research Service. Another set of equations has been developed by Marks et al. (1998).

Walls and Scott (1996) compared predictions from the PMP with observations of *E. coli* O157:H7 growth in ground beef and concluded that the PMP "offers reasonably good predictions of growth in raw ground beef" (p. 1,335). Table 3-15 compares the predictions from the Marks et al. (1998) equations with the predictions from the PMP (Buchanan and Bagi 1994) and the Walls and Scott (1996) observations. Both sets of predictions gave similar results, although the Marks et al. (1998) equations gave closer predictions to lag time and generation time.

TABLE 3-15 Comparison of Pathogen Modeling Program (PMP) with Marks et al. (1998) Equations Using Walls and Scott (1996) Observations

Growth Conditions		Generation Time (hours)			Lag Period Duration (hours)			T1000 (hours)—Time for 3 Log Increase in *E. coli* O157:H7 Organisms		
Temp	pH	Walls and Scott (1996)	PMP	Marks et al. (1998)	Walls and Scott (1996)	PMP	Marks et al. (1998)	Walls and Scott (1996)	PMP	Marks et al. (1998)
12°C	5.7	6.00	3.80	3.62	16.20	30.50	26.99	76.70	68.50	63.19
12°C	6.3	3.90	3.20	3.62	2.78	27.20	26.99	38.60	59.50	63.19
20°C	5.7	1.50	1.00	1.11	2.08	8.34	6.83	17.60	18.30	17.96
20°C	6.3	1.30	1.00	1.11	1.25	7.54	6.83	14.40	17.30	17.96
35°C	5.7	0.40	0.30	0.38	1.23	1.53	1.52	5.00	4.80	5.29
35°C	6.3	0.40	0.30	0.38	1.05	1.40	1.52	5.10	4.60	5.29

The Marks et al. (1998) equations used temperature as the only parameter. Since a single parameter model requires less information, and since these equations also included adjustments for the variability inherent in the system, these are the ones used in the model. Given a temperature (τ) in °C, the following sets of equations are used to predict growth of *E. coli* O157:H7 in ground beef:

Lag period duration (LPD) is calculated as follows:

$$\ln(\text{LPD}) = 9.98 + [-2.69 \times \ln(\tau)] \tag{3.27}$$

ln(LPD) has a standard deviation of 0.27. Consequently, the distribution is modeled as $\ln(\text{LPD}) \sim \text{normal}\ \{9.98 + [-2.69 \times \ln(\tau), 0.27]\}$.

Generation time (GT) is calculated as follows:

$$\ln(\text{GT}) = 7.03 + \{-6.31 \times \ln[\ln(\tau)]\} \tag{3.28}$$

ln(GT) has a standard deviation of 0.16. Consequently, the distribution is modeled as $\ln(\text{GT}) \sim \text{normal}\ (7.03 + \{-6.31 \times \ln[\ln(\tau)]\}, 0.16)$.

The maximum population density (MPD) (e.g., the maximum number of *E. coli* O157:H7 organisms) is calculated as follows:

$$MPD = TMD + (-0.014 \times \tau) \quad (3.29)$$

The theoretic maximum density (TMD) at refrigeration temperatures was estimated by Marks et al. (1998) to be about 10 logs. Walls and Scott (1996) also demonstrated growth in ground beef up to 10 logs. However, the maximum growth of *E. coli* O157:H7 achievable in ground beef is also thought to be a function of the total microbial population density in the food. Such a phenomenon has been demonstrated for *Salmonella* where the suppression of growth of all microorganisms in the food occurred when the total microbial population achieved the MPD characteristic of the food (Jameson 1962). This effect has also been reported for *S. aureus*, *L. monocytogenes*, and *Carnobacterium* spp. (Buchanan and Bagi 1997; Duffes et al. 1999; Nilsson et al. 1999; Ross and McMeekin 1991; Grau and Vanderlinde 1992).

Because maximum growth of *E. coli* O157:H7 possible in a food depends on the population of all microbes, and the population of other microbes in ground beef varies, it is assumed that the TMD varies. A triangular distribution is used to model this variability, where the minimum TMD is assumed to be 5 logs, the maximum TMD is assumed to be 10 logs, and the most likely TMD is uncertain but can range uniformly from 5 to 10 logs.

From Marks et al. (1998), the MPD has a standard deviation of 0.15 and is thus modeled as follows:

$$MPD = \text{normal}\{\text{triangular}[5, \text{uniform}(5,10), 10] + (-0.014 \times \tau), 0.15\} \quad (3.30)$$

Output from a Monte Carlo simulation of these equations overlaps most of the observations from Walls and Scott (1996) with three exceptions: the prediction of the lag period duration (1) for a temperature of 12°C (54°F) at a pH of 6.3, (2) for a temperature of 20°C (68°F) with a pH of 5.7, and (3) for a temperature of 20°C (68°F) with a pH of 6.3. In each case, the equations overestimate the lag period duration. Nevertheless, the T1000 times, which incorporate both the LPD and GT, overlap the Walls and Scott (1996) observations for all conditions.

Continued research of the effect of various storage condition combinations (e.g., pH, moisture, packaging, freezing, refrigeration, thawing) on *E. coli* O157:H7 levels in ground beef products would allow construction of better predictive microbial models. Incorporation of such models into risk assessment is further dependent on studies to develop frequency distributions for various storage conditions.

Modeling Storage Temperature

As noted in Figure 3-22, this model includes the effects of storage temperature on the increase or decrease of *E. coli* O157:H7 in ground beef at three steps: (1) retail or wholesale storage, (2) transportation to the location of preparation (i.e., home or HRI), and (3) storage before cooking. Temperatures for all three steps are based on internal product temperatures of ground beef taken on nearly 1,000 samples (Audits International 1999). Table 3-16 shows numbers of occurrences of storage temperatures above 45°F.

The model assumes that *E. coli* O157:H7 levels do not increase at refrigeration temperatures below 45°F based on Palumbo (1997) and input from the National Advisory Committee on Microbiological Criteria for Food (NACMCF 1999).

Temperature at each step (τ_{S2}, τ_{S3}, τ_{S4}) is modeled as a cumulative distribution in the following form:

TABLE 3-16 Storage Temperatures above 45°F

	Step 2 Retail/Wholesale Storage	Step 3 Transport	Step 4 Home/HRI Storage
Total samples	975	971	939
Temperature (°F)	Number of Samples above 45°F		
46	49	175	47
49	49	223	28
52	8	68	4
55	4	49	5
58	2	19	4
61	0	19	1
64	0	3	0
67	0	2	1
70	0	1	1

Source: Audits International 1999.

$$\tau_{SX} = \text{cumulative [(temperature), (}p\text{)]} \quad (3.31)$$

The cumulative distribution in Equation 3.31 consists of two arrays: the first array represents various temperatures shown in Table 3-16, and the second array represents the corresponding cumulative probability of each of the temperatures. In addition to modeling the variability in storage temperature as a cumulative distribution, uncertainty regarding the actual frequency of each temperature is modeled using a beta distribution after a method reported by Vose (1999).

Modeling Storage Time

The amount of time at each step (T_2, T_3, T_4) that ground beef is stored at a given temperature determines how much growth of *E. coli* O157:H7 takes place. Although there are recommendations for how long ground beef may be stored at temperatures above 45°F (FDA 1997), there are no data documenting this length of time. FSIS recommends that ground beef be stored in the refrigerator for no more than 2 days (FSIS 2000). For Steps 2 and 4, time of storage is modeled as an exponential distribution with a mean of 1. An exponential distribution was chosen because it has a single parameter and its probability density function is monotonically decreasing. In other words, using this function assumes that on average, ground beef is more likely to be stored for shorter times than for longer times. An exponential distribution with a mean of 1 predicts that 99% of ground beef will be stored less than 4.6 days. Additionally, uncertainty about the mean of the exponential distribution is modeled using a uniform distribution from 0.5 days to 1.5 days. An exponential distribution with a mean of 0.5 predicts that 99% of ground beef will be stored less than 2.3 days, while an exponential distribution with a mean of 1.5 predicts that 99% of ground beef will be stored less than 6.9 days. Equation 3.32 shows how time is modeled across the various uncertainties for Steps 2 and 4.

$$T_X = \text{exponential [uniform(0.5, 1.5)]} \quad (3.32)$$

For Step 3, the time of storage for transportation is based on data from Audits International (1999) (Table 3-17).

TABLE 3-17 Time of Transport from Retail to Home

Time of Transport	Number of Observations
0.00	36
0.25	5
0.50	46
0.75	168
1.00	240
1.25	210
1.50	156
1.75	67
2.00	28
2.25	10
2.50	8
2.75	3
3.00	1
6.50	1

Source: Audits International 1999.

In Step 3, time (T_3) is modeled as a cumulative distribution in the following form:

$$T_3 = \text{cumulative}[(\text{time}), (\text{p})] \tag{3.33}$$

As with Equation 3.31, the cumulative distribution in Equation 3.33 consists of two arrays. The first array represents the times shown in Table 3-17, and the second array represents the corresponding cumulative probability of each of the times. Again, uncertainty regarding the actual frequency of each time is modeled using a beta distribution after a method reported by Vose (1999).

Modeling the Effect of Freezing

Some ground beef may be frozen during storage and transportation. A decline in *E. coli* O157:H7 levels between 0 and 3 logs per gram of frozen ground beef is modeled based on laboratory studies of the effects of freezing on *E. coli* O157:H7 levels in ground beef (Ansay et al. 1999; Sage and Ingham 1998). Table 3-18 shows the frequency distribution used to model the log reduction of *E. coli* O157:H7 due to freezing. Uncertainty regarding the proportion of ground beef that is frozen is modeled uniformly from 20% to 80%.

Modeling Growth for a Single Step

Step 2 provides the first opportunity for *E. coli* O157:H7 growth. First, ln(LPD) is calculated given τ_{S2} using Equation 3.27. The lag period for Step 2 (LPD_2) is compared with the amount of time in Step 2 (T_2). If $LPD_2 < T_2$, then no growth occurs and the cumulative lag used in Step 2 (CLU_2) is as follows:

TABLE 3-18 Frequency Distribution for Log Reduction in *E. coli* O157:H7 due to Freezing

Log Reduction	Frequency
0.0	0.000
0.5	0.000
1.0	0.190
1.5	0.580
2.0	0.170
2.5	0.028
3.0	0.028

$$CLU_2 = \frac{LPD_2}{T_2} \tag{3.34}$$

If $LPD_2 > T_2$, then the amount of time available for growth equals $LPD_2 - T_2$. Equation 3.28 calculates $\ln(GT_2)$ given τ_{S2}. The log of growth for Step 2 (G_2) is then calculated as follows:

$$G_2 = \log_{10}\left(e^{\frac{LPD_2 - T_2}{GT_2}}\right) \tag{3.35}$$

CLU_2 or G_2 are only calculated if τ_{S2} is greater than 45°F. Otherwise both CLU_2 and G_2 are set at 0.

Since the CLU is modeled as a percentage that can increase across each step, the amount of *E. coli* O157:H7 growth in Steps 3 and 4 is also dependent on the CLU. If CLU_2 is greater than 0, then the LPD in Step 3 must be adjusted to account for the CLU. The adjusted LPD_3 (LPD_{3a}) is calculated by $LPD_3 \times (1 - CLU_2)$. Equations 3.34 and 3.35 can then be used to calculate G_3 by substituting LPD_{3a} where LPD_3 would occur. The amount of *E. coli* O157:H7 growth in Step 4 would be calculated in the same manner.

Modeling Growth across Steps 2 to 4

Since CLU and G are only modeled when storage temperature exceeds 45°F, there is a set of eight potential growth combinations that can occur in Steps 2 through 4 for a single ground beef serving. If the temperature of the ground beef serving is below 45°F, then growth is not modeled. If the serving is exposed to temperatures above 45°F in one of the three steps, then CLU and/or G is calculated for that step. If the temperature of the serving is above 45°F in two of the steps, then CLU and/or G is calculated for that step and an adjusted LPD is calculated if CLU is less than 1. The same principle applies if the temperature of the uncooked ground beef serving is above 45°F in all three steps. Thus, the total number of combinations of steps above or below 45°F is 2^3 or 8. The probability that a serving will be exposed to a particular combination of steps above 45°F is dependent on the probability of each step being above 45°F. These probabilities are considered fixed but uncertain.

The probability that a serving in a particular step will be above 45°F is modeled using a beta(s+1,n–s+1) distribution incorporating the data in Table 3-16, where s equals the total samples above 45°F and n equals the total samples. Consequently, a single simulation of the model will generate eight different growth distributions for each of the eight different combinations of steps above 45°F. The eight growth distributions generated from these eight

combinations are integrated across the probabilities of their occurrence to create an overall growth distribution for *E. coli* O157:H7 in stored ground beef. This distribution is then integrated with the distribution for freezing of ground beef to give a final distribution (G_{pop}) representing the change of *E. coli* O157:H7 due to storage in Steps 2 to 4 for all servings.

Figure 3-23 shows the results of 20 Monte Carlo simulations where G_{pop} is estimated. Each line represents the frequency distribution returned by a single simulation.

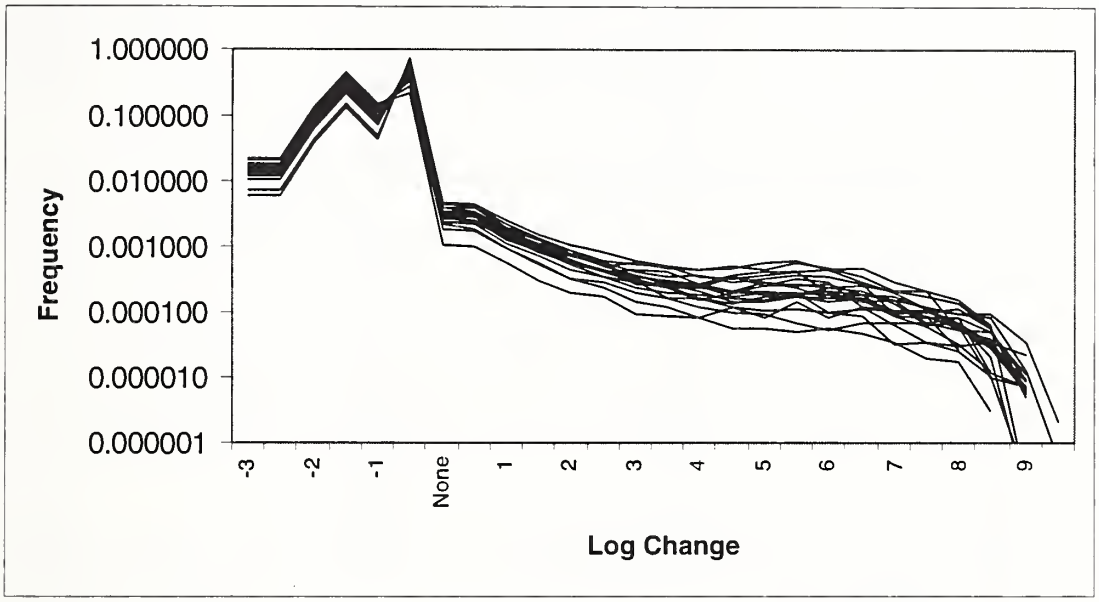

FIGURE 3-23 Frequency of log increase or log decrease due to storage for 20 simulations.

Cooking (Step 5)

Step 5 simulates the effect of cooking on ground beef in homes and HRI. Nearly all ground beef is cooked. The effect of cooking is dependent on the cooking temperature, the storage temperature prior to cooking, and the thermodynamics of the product. The effects of cooking temperature and precooking storage are modeled. Cooking is modeled by relating log reduction to internal product temperatures.

Temperatures of Cooked Ground Beef

The temperature to which a ground beef serving is cooked is based on a survey of final internal product temperatures of cooked hamburger patties prior to consumption (Audits International 1999). Table 3-19 shows the internal hamburger temperatures reported. Because visual cues are unreliable indicators of cooking of ground beef (Liu and Berry 1996; Van Laack et al. 1996), quantitative time-temperature cooking data were used (Audits International 1999) rather than consumer behavior survey data (Brent 1999).

TABLE 3-19 Internal Temperatures of Cooked Hamburger Patties

Internal Temperature (°C)	Observations (n)	Internal Temperature (°C)	Observations (n)
39	2	69	22
41	5	71	18
43	3	73	55
45	9	75	45
47	5	77	59
49	14	79	19
51	8	81	18
53	13	83	74
55	23	85	11
57	12	87	5
59	20	89	9
61	31	91	1
63	41	93	3
65	25	95	3
67	41	Total	594

Source: Audits International 1999.

Effect of Cooking

Juneja et al. (1997) determined the effect of cooking on hamburgers experimentally inoculated with an initial load of 6.6 logs of *E. coli* O157:H7. Final internal temperatures of the hamburgers ranged from 56°C to 74°C (133°F to 166°F). The log of the surviving *E. coli* O157:H7 was then measured. Given a temperature in Fahrenheit (τf), the following linear regression equation gives the corresponding ($r^2 = 0.94$) log reduction:

$$LR = 6.6 - (20.53 - 0.12 \times \tau f) \quad (3.36)$$

Juneja et al. (1997) noted that 73% lean ground beef patties (100 grams) cooked to an internal temperature of 68.3°C (155°F) would have a 4 log reduction of a five strain cocktail of *E. coli* O157:H7. This is consistent with a report by Jackson et al. (1996) that 78% lean ground beef patties (114 grams) inoculated with about 6 logs of bacteria and cooked to an internal temperature of 68.3°C (155°F) would have a 4.1 log reduction with a standard deviation of 0.5 logs. In both studies, inoculated hamburgers were stored under refrigeration.

Semanchek and Golden (1998) reported variability in heat resistance among three strains of *E. coli* O157:H7 and concluded that "exposure to different environments may select for resistance to suboptimum conditions or subsequent stress" (p. 399). Jackson et al. (1996) reported that the response of *E. coli* O157:H7 to cooking appeared to be related to original storage temperatures. *E. coli* O157:H7 in frozen ground beef was more heat resistant than *E. coli* O157:H7 in ground beef refrigerated or stored at higher temperatures. Jackson et al. reported

results from 27 different combinations of storage conditions and cooking temperatures (listed in Table 3-20).

TABLE 3-20 Mean Log Reductions (± Sample Standard Deviation [std. dev.]) of *E. coli* O157:H7 in Grilled Ground Beef Patties

Pretreatment Storage Conditions	Internal Cooking Temperature					
	54.4°C		62.8°C		68.3°C	
	Mean LR	Std. Dev.	Mean LR	Std. Dev	Mean LR	Std. Dev
–18°C, 8 days	0.3	0.1	1.2	0.6	3.0	1.8
–18°C, 8 days followed by 21°C, 4 hours	0.7	0.1	3.9	0.9	4.8	0.3
–18°C, 8 days followed by 30°C, 4 hours	1.6	0.7	5.5	0.3	5.2	0.7
3°C, 9 hours	0.5	0.3	2.6	0.5	4.1	0.5
3°C, 9 hours followed by 21°C, 4 hours	1.3	0.4	5.3	0.2	5.2	0.3
3°C, 9 hours followed by 30°C, 4 hours	1.9	0.3	6.0	0.2	5.8	0.4
15°C, 9 hours	1.0	0.1	4.3	0.7	5.1	0.1
15°C, 9 hours followed by 21°C, 4 hours	1.6	0.8	5.4	0.5	5.6	0.4
15°C, 9 hours followed by 30°C, 4 hours	2.4	0.1	5.3	1.7	6.4	0.2

Source: Jackson et al. 1996.

Modeling Cooking

The effect of cooking is calculated in the model by applying log reductions for the range of cooking temperatures shown in Table 3-19. Although Jackson et al. do not report on the effect of cooking at temperatures greater than 68.3°C (155°F), this effect was extrapolated in accordance with the linear relationship demonstrated by Juneja et al. (1997).

Figure 3-24 depicts the variability expected for log reductions across the nine different pretreatments shown in Table 3-20. Individual lines are not labeled, as the purpose of the chart is to show the wide range of variability in log reduction based solely on precooking storage.

The information in Table 3-20 is used to calculate a linear regression equation for each of the nine pretreatments with estimated y intercept (α), slope (β), and the standard error of y (stey) terms. For each regression equation, the probability of a particular log reduction for each of the 30 temperatures (τ) in Table 3-19 is calculated using the Excel Normdist function:

$$p(\text{LR} \mid \tau) = \text{NORMDIST}(\text{LR}, \alpha + \beta \times \tau, \text{stey}, 1) \quad (3.37)$$

Integrating the probabilities of all of the temperatures and the probability of a given log reduction across all τ results in a log reduction curve for a given pretreatment:

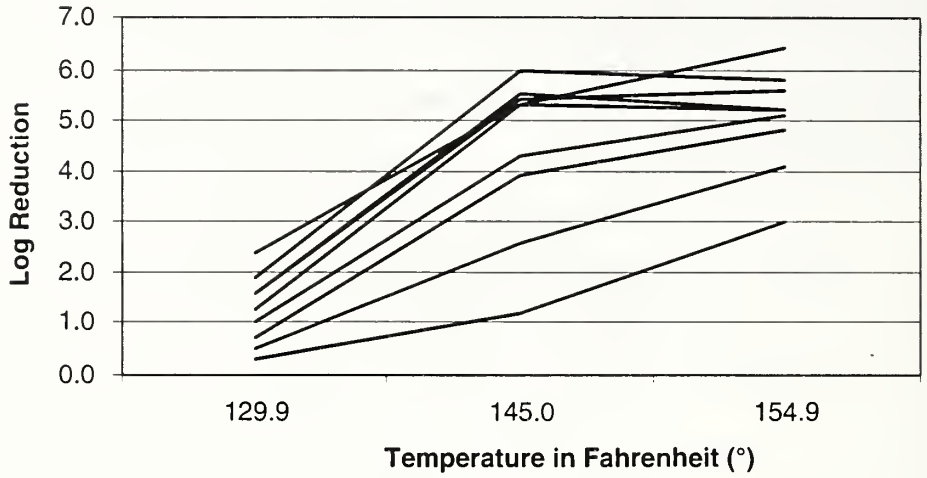

FIGURE 3-24 Variability in log reduction of *E. coli* O157:H7 for nine different pretreatments based on Jackson et al. (1996).

$$f(\mathrm{LR}) = \int_{39}^{95} (p(\mathrm{LR} \mid \tau) \times \infty p(\tau) d\tau \tag{3.38}$$

The probability of a particular pretreatment occurring for a ground beef serving is fixed but uncertain. These probabilities are dependent on probabilities used in Steps 2 to 4. For instance, the probability of the serving having undergone freezing before cooking is dependent on, and correlated with, the probability that the serving was frozen during Steps 2 to 4.

The log reduction curves for each of the nine pretreatments are integrated to create a single log reduction curve. This log reduction curve (LR_{pop}) describes the frequency of log reductions from cooking for the entire population of servings and is estimated using Monte Carlo methods.

Figure 3-25 shows 20 different LR_{pop} curves calculated from Monte Carlo simulations.

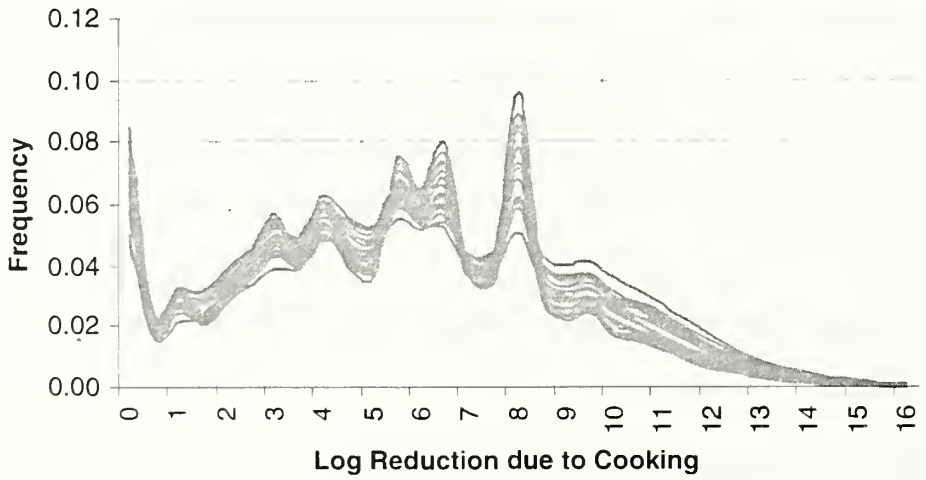

FIGURE 3-25 Frequency of log reduction due to cooking for 20 simulations.

Note that considerable uncertainty exists regarding the log reduction due to cooking. Note also that this particular set of simulations suggests that between 4% and 8% of servings have no log reduction applied.[2]

Food items with ground beef as a major ingredient were assumed to have cooking practices that parallel cooking practices for hamburgers. As noted in the scope, cooking of ground beef as an ingredient in products such as chili, spaghetti, and soup is assumed to destroy all *E. coli* O157:H7 in the product. Such ground beef is usually precooked in a granular form and then subjected to further cooking.

Although D'Sa et al. (2000) have reported a difference in log reductions between single-sided and double-sided cooking, this distinction was not modeled. Results from Juneja et al. (1997), Jackson et al. (1996), and D'Sa et al. (2000) were based on cooking similar sized hamburger patties of relatively uniform thickness. Consequently, this model did not explicitly account for differences in patty thickness. Nevertheless, the variability of internal cooking temperatures included in this model should account for the thermodynamics in ground beef servings with varying thickness.

Consumption (Step 6)

Types of Ground Beef Products Modeled

Ground beef is consumed in the United States as the main course of a meal or as an ingredient in a recipe both at home and away from home in HRI. Data from the 1994–1996, 1998 CSFII were used to model ground beef consumption patterns by age of the consumer and location where the meal was consumed. The CSFII is a national survey of U.S. food intakes that consists of the following:

- a nationally representative sample of 21,154 respondents;
- two 24-hour recalls of foods eaten during two nonconsecutive days (with the interview for the second day conducted on a different day of the week, 3 to 10 days after the interview for the first day);
- demographic information on consumers;
- location where the meal was consumed (i.e., home versus away from home); and
- annual and 4-year survey weights to reflect the consumption patterns of the noninstitutional U.S. population.

Three categories of ground beef meals were considered in this step: (1) raw ground beef, (2) hamburger patties and sandwiches, and (3) formed ground beef products in which the ground beef is a major ingredient to the product (e.g., meatballs and meat loaf). Food items for each category were selected from over 7,200 food items within the 1994–1996 and 1998 CSFII (Kause 2001). Tables 3-21, 3-22, and 3-23 provide detailed information on the food items that comprise each ground beef category. Only food items with at least one eating occasion between 1994 and 1996 or in 1998 were included.

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[2]The 1994–1996, 1998 CSFII included four individuals (three between 25 and 64 years of age and one less than 5 years of age) who were reported to have consumed "raw" ground beef. These reported ground beef servings comprised less than 0.07% of the estimated annual number of ground beef servings consumed in the United States (Tables 3-24, 3-25, and 3-26). For modeling purposes, these servings are considered to be a subset of those servings that have no log reduction in *E. coli* O157:H7 during cooking (e.g., grossly undercooked servings).

TABLE 3-21 1994–96, 1998 CSFII Food Codes for Raw Ground Beef Meals

Food Code	Food Item
21500000	Raw ground beef
27116400	Steak tartare (raw ground beef and egg)

Amounts of Ground Beef Products Consumed

The amount of ground beef in each food item was calculated using the CSFII recipe files (Tables 3-24, 3-25, and 3-26). This provides information on the amount of ground beef consumed during a meal (e.g., meatball and spaghetti dinner).

Consumption data for each ground beef category were stratified by general location of where the meal was eaten (i.e., either at home or away from home). This resulted in six combinations for ground beef consumption by location: (1) raw ground beef consumed within the home, (2) raw ground beef consumed away from the home in HRI, (3) ground beef consumed as hamburgers within the home, (4) ground beef consumed as hamburgers away from the home in HRI, (5) ground beef used as a primary ingredient in a recipe (e.g., meatballs or meat loaf) within homes, and (6) ground beef used as an ingredient in a recipe (e.g., meatballs or meat loaf) away from the home.

Ground beef consumption was further stratified into four age categories (0 to 5, 6 to 24, 25 to 64, and 65+ years of age)[3] to provide more detail on exposure of susceptible age groups (0 to 5 and 65+ years of age). The age-specific annual number of ground beef meals consumed and the corresponding serving size (in grams) was calculated using SAS (version 8.0) and WesVar (version 2.0) software (Kause 2001). The following information was derived:

- weighted descriptive statistics (e.g., mean amount eaten in grams, number of eating occasions, and mean number of eating occasions) that characterize all age/location/food category-specific eating occasions consumed in two nonconsecutive days of eating;
- distributions of the amount of food (in grams) that is eaten at all eating occasions, expressed as weighted percentiles after adjustment for the stratified sample design using a jackknife procedure in the WesVarPC software package with replicate weights that accompany the 1994–96, 1998 CSFII data;
- weighted descriptive statistics to describe the amount of food (in grams) that is eaten per person per day and the number of consumers; and
- per capita estimates of food eaten.

The resulting number of servings and mean serving size of ground beef by age and location for each ground beef category are shown in Tables 3-24, 3-25, and 3-26. These ground beef meals account for over 18 billion ground beef servings consumed annually in the United States.

[3]Age categories were used instead of age-specific data because of the limited number of observations for each age (e.g., 1-year-olds, 2-year-olds, etc.) to derive the statistics.

TABLE 3-22 1994–96, 1998 CSFII Food Codes for Hamburger Patty and Sandwich Meals

Food Code	Food Item	Food Code	Food Item
21500100	Ground beef or patty	27510390	Double bacon cheeseburger, on bun
21500200	Ground beef or patty, breaded, cooked	27510400	Bacon cheeseburger, ¼ lb meat, with tomato, on bun
21501000	Ground beef, regular, cooked	27510420	Taco burger, on bun (include chiliburger with cheese)
21501200	Ground beef, lean, cooked	27510430	Double bacon cheeseburger, with mayo, tomato, on bun
21501300	Ground beef, extra lean, cooked	27510440	Bacon cheeseburger, ¼ lb, with mayo and tomato, on bun
25220140	Beef sausage, fresh, bulk, patty or link, cooked	27510480	Cheeseburger, with onions, on rye bun
27510210	Cheeseburger, plain, on bun	27510500	Hamburger, plain, on bun
27510220	Cheeseburger, with mayo, on bun	27510510	Hamburger, with tomato and or catsup, on bun
27510230	Cheeseburger, with mayo and tomato, on bun	27510520	Hamburger, with mayo and tomato, on bun
27510240	Cheeseburger, ¼ lb meat, plain, on bun	27510530	Hamburger, ¼ lb meat, plain, on bun
27510250	Cheeseburger, ¼ lb meat, with mayo, on bun	27510540	Double hamburger with tomato and or catsup, on bun
27510260	Cheeseburger, ¼ lb meat, with mushroom sauce, on bun	27510550	Double hamburger with mayo and tomato, double-decker bun
27510270	Double cheeseburger, plain, on bun	27510560	Hamburger, ¼ lb meat with mayo and tomato, on bun
27510280	Double cheeseburger, with mayo, on bun	27510590	Hamburger, with mayo, on bun
27510300	Double cheeseburger, with mayo, on double-decker bun	27510600	Hamburger, 1 oz meat, plain, on miniature bun
27510310	Cheeseburger, with tomato and or catsup, on bun	27510610	Hamburger, 1 oz meat, tomato, on miniature bun
27510311	Cheeseburger, 1 oz meat, plain, on mini bun	27510620	Hamburger, ¼ lb meat, with tomato and or catsup, bun
27510320	Cheeseburger, ¼ lb meat, with tomato/catsup, bun	27510630	Hamburger, ¼ lb meat, with mayo, on bun
27510330	Double cheeseburger, with tomato and or catsup, on bun	27510640	Hamburger, ¼ lb meat (modified fat) with tomato, on bun
27510340	Double cheeseburger, with mayo and tomato on bun	27510670	Double hamburger, with mayo and tomato, on bun
27510350	Cheeseburger, ¼ lb meat, with mayo and tomato on bun	27510680	Double hamburger (1/2 lb meat), with tomato/catsup, bun
27510360	Cheeseburger, with mayo, tomato and bacon on bun	27510690	Double hamburger, 1/2 lb meat, with mayo and tomato/catsup, bun
27510370	Double cheeseburger with mayonnaise, on bun	27510700	Meatball and spaghetti sauce submarine sandwich
27510380	Triple cheeseburger with mayo, tomato, on bun		

TABLE 3-23 1994–96, 1998 CSFII Food Codes for Other Ground Beef-Based Meals

Food Codes	Food Item
21500110	Ground beef, meatballs, meat only, not specified as to regular/lean
21540100	Ground beef with textured vegetable protein, cooked
23220010	Veal, ground or patty, cooked
27116350	Stewed, seasoned ground beef, Mexican style
27118110	Meatballs, p.r. (albondigas)
27118120	Stewed, seasoned ground beef, Puerto Rican style
27160100	Meatballs, not specified as to type of meat, with sauce
27161010	Meat loaf, p.r. (albondigon)
27214100	Meat loaf made with beef
27214110	Meat loaf with beef, with tomato sauce
27260010	Meat loaf, not specified as to type of meat
27260050	Meatballs, with breading, with gravy
27260080	Meat loaf made with beef and pork
27260090	Meat loaf with beef, veal and pork
27260100	Meat loaf with beef and pork, with tomato sauce
27113300	Swedish meatballs with cream or white sauce (mixture)

TABLE 3-24 Annual Number of Servings of Raw Ground Beef Consumed at Home and Away from Home by Age Category in the 1994–1996, 1998 CSFII

Age in Years	Number of Servings	Mean Serving Size (grams)
Home		
0–5	—	—
6–24	—	—
25–64	8,861,470	113.40
65+	—	—
Total	8,861,470	
Away from Home		
0–5	522,315	56.70
6–24	—	—
25–64	3,883,053	12.60
65+	—	—
Total	4,405,368	

TABLE 3-25 Annual Number of Servings of Hamburger Patties and Sandwiches Consumed at Home and Away from Home by Age Category in the 1994–1996, 1998 CSFII

Age in Years	Number of Servings	Mean Serving Size (grams)
Home		
0–5	395,592,840	51.86
6–24	1,478,341,250	95.17
25–64	2,517,532,750	102.02
65+	577,825,295	86.52
Total	4,969,292,135	
Away from Home		
0–5	717,308,950	36.88
6–24	4,215,244,840	78.73
25–64	5,628,291,058	87.64
65+	523,589,763	67.53
Total	11,084,434,611	

TABLE 3-26 Annual Number of Servings of Ground Beef-Based Meals (Such as Meat loaf and Meatballs) Consumed at Home and Away from Home by Age Category in the 1994–1996, 1998 CSFII

Age in Years	Number of Servings	Mean Serving Size (grams)
Home		
0–5	109,001,410	62.36
6–24	362,621,113	123.02
25–64	686,647,125	123.95
65+	272,269,925	100.09
Total	1,430,539,573	
Away from Home		
0–5	27,548,375	64.01
6–24	169,672,623	75.64
25–64	398,076,300	101.57
65+	135,376,128	67.30
Total	730,673,425	

Determining Exposures to E. coli O157:H7

The amount of *E. coli* O157:H7 to which a consumer is exposed in a single serving of ground beef is a function of the original number of *E. coli* O157:H7 organisms and the subsequent effects of storage, handling, and cooking on the growth or decline in the number of *E. coli* O157:H7 organisms in ground beef. The effect of storage on the growth or decline of organisms has been determined in Steps 2 to 4, and the effect of cooking has been determined in Step 5. The original number of organisms in a product is determined by the original concentration after grinding (Step 1) and the amount of product consumed (Step 6).

Equation 3.39 calculates the number of *E. coli* O157:H7 in a grinder load. The concentration in the grinder load (GLC) is calculated by dividing the total number of *E. coli* O157:H7 organisms (ECO) by the weight of the grinder load in grams as shown in the following equation where NCB is the number of combo bins in the grinder load, 2,000 is the weight of a combo bin in pounds, and 454 is the number of grams in a pound:

$$\mathrm{GLC} = \frac{\mathrm{ECO}}{\mathrm{NCB} \times 2{,}000 \times 454} \tag{3.39}$$

For a given GLC and a given serving size (WTG) the probability of having a particular number of organisms (BACT) in a serving is predicted by assuming a Poisson distribution

$$p(\mathrm{BACT}) = \frac{(\mathrm{GLC} \times \mathrm{WTG})^{\mathrm{BACT}}}{\mathrm{BACT!}} e^{-\mathrm{GLC} \times \mathrm{WTG}} \tag{3.40}$$

Integrating the probabilities of all GLCs and the probability of all BACTs across all WTGs results in an initial serving distribution:

$$f(\mathrm{BACT}) = \int_{\mathrm{GLC}=10^{-7}}^{10^{7}} \int_{\mathrm{WTG}=12}^{124} [p(\mathrm{BACT} \mid \mathrm{GLC}, \mathrm{WTG}) \times p(\mathrm{GLC}) \times p(\mathrm{WTG})\, d\mathrm{GLC}\, d\mathrm{WTG}] \tag{3.41}$$

This initial serving distribution describes the frequency of *E. coli* O157:H7 levels in all ground beef servings before storage and cooking ($\mathrm{BACT}_{\mathrm{pop}}$). This distribution is estimated for both the low prevalence and high prevalence seasons. Figure 3-26 shows the results of 20 Monte Carlo simulations where $\mathrm{BACT}_{\mathrm{pop}}$ is estimated for the low prevalence season and the high prevalence season.

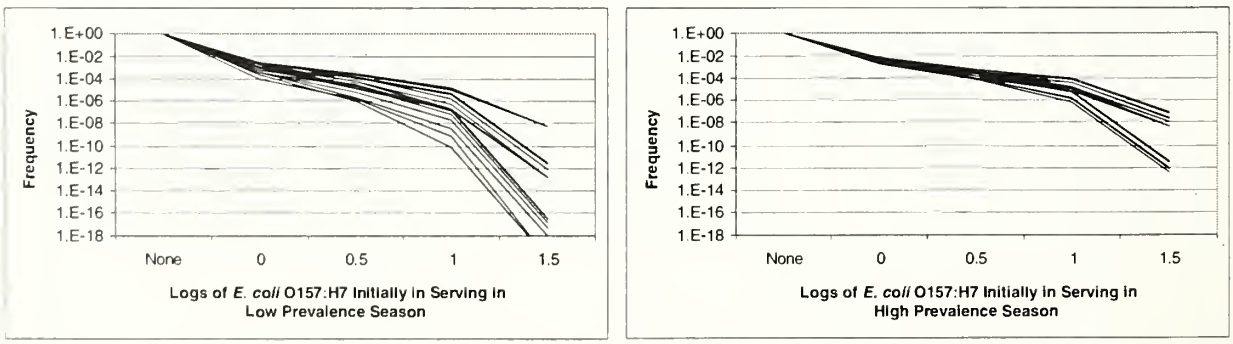

FIGURE 3-26 Frequency of logs of *E. coli* O157:H7 initially present in servings for low prevalence and high prevalence seasons.

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4

Hazard Characterization

This chapter describes the process used to characterize the number of symptomatic infections resulting from the consumption of cooked ground beef servings contaminated with *Escherichia coli* O157:H7. This process is commonly referred to as a dose-response assessment. Unlike many chemical hazards and some pathogens, the dose-response relationship for *E. coli* O157:H7 is unknown. Limited dose-response information is available from an animal study conducted by Pai et al. (1986), in which infant rabbits were exposed to *E. coli* O157:H7. Because there is no effective treatment for *E. coli* O157:H7 infection and the outcome of infection can include severe illness and death, experimental studies exposing humans to *E. coli* O157:H7 have not been, and probably never will be, performed. In contrast, a substantial amount of surveillance data exist on the annual number of illnesses due to infection with *E. coli* O157:H7. Thus, this risk assessment uses a multistep process to derive a dose-response function for E. *coli* O157:H7 (Figure 4-1). This process is divided into four primary steps: (1) estimation of the number of *E. coli* O157:H7-related illnesses attributable to the consumption of contaminated ground beef (response); (2) estimation of the likelihood and level of *E. coli* O157:H7 in cooked ground beef servings (dose, derived in Chapter 3); (3) derivation of upper and lower bounds for the *E. coli* O157:H7 dose-response function based on clinical studies of surrogate pathogens; and (4) derivation of the "most likely" (50th percentile) dose-response function for *E. coli* O157:H7 (Powell et al. 2000).

This chapter begins by estimating a baseline annual number of illnesses of *E. coli* O157:H7 infection from all exposures using data from the Emerging Infections Program, Foodborne Disease Active Surveillance Network (FoodNet). This baseline annual number of cases is adjusted upward to account for underdiagnosis and underreporting, providing an estimated total annual number of cases of symptomatic *E. coli* O157:H7 infection for the United States. Then, using data from studies of sporadic cases of *E. coli* O157:H7 infection and outbreaks of *E. coli* O157:H7, the proportion of total cases due to ground beef exposure is derived. Next, lower and upper bound dose-response functions are constructed using foodborne pathogens other than *E coli* O157:H7. These lower and upper bound dose response functions are used in combination with the estimated number of cases due to ground beef and the estimated number of ground beef

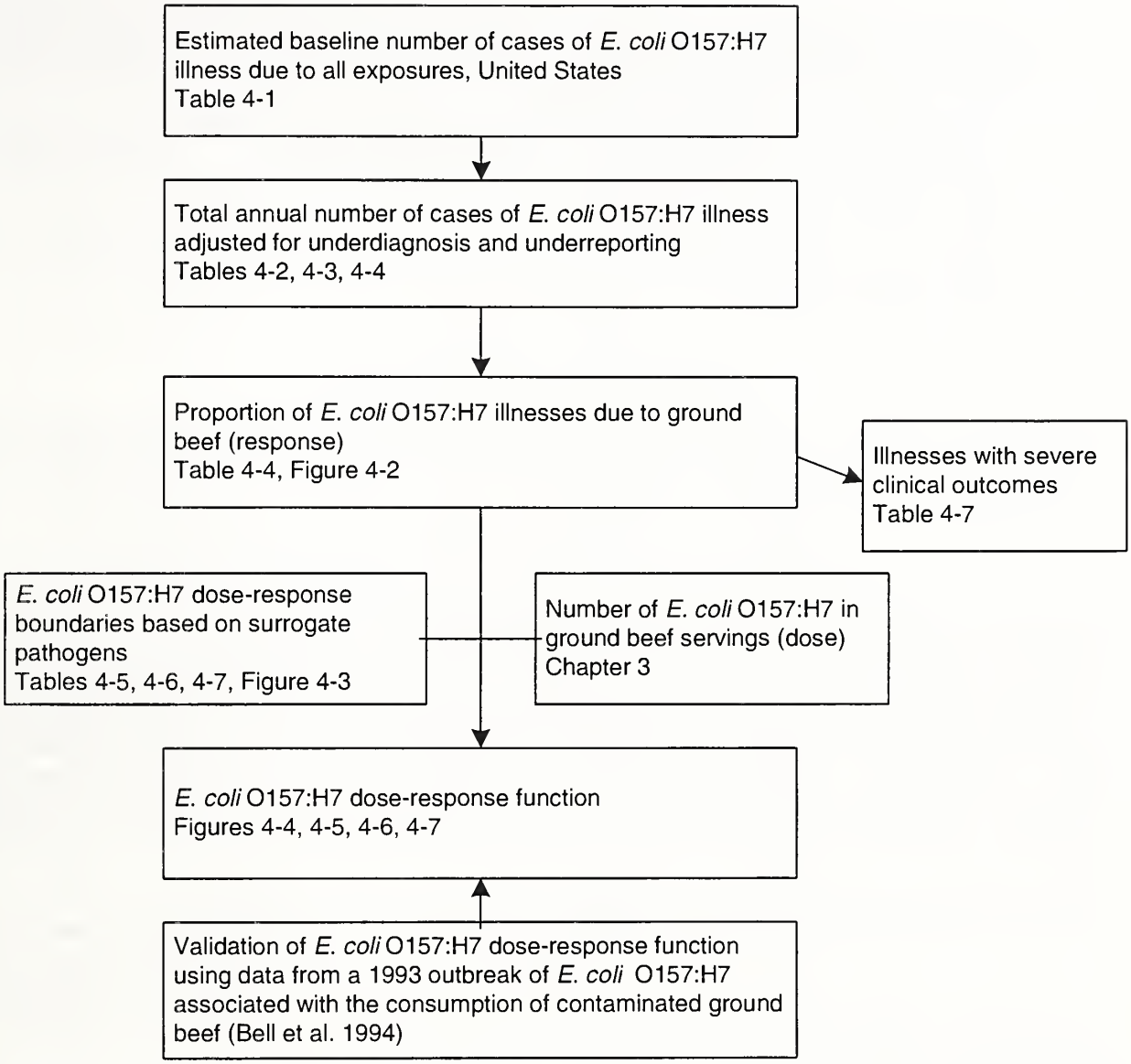

FIGURE 4-1 Flowchart for the derivation of the dose-response function for *E. coli* O157:H7 in ground beef.

servings contaminated with *E. coli* O157:H7 to generate a dose-response function for *E. coli* O157:H7. Finally, dose and response information from an outbreak of *E. coli* O157:H7 due to contaminated ground beef is compared with the *E. coli* O157:H7 dose-response function.

DEFINITION OF KEY TERMS

The following key terms are used throughout this chapter:

- Dose is the number of *E. coli* O157:H7 organisms in a serving of ground beef.
- Response refers to the number and severity of illnesses resulting from consumption of ground beef servings contaminated with *E. coli* O157:H7.

- Dose-response function refers to the mathematical relationship between the consumption of a ground beef serving containing a specific number (dose) of organisms and the resulting number of illnesses (response).
- Surrogate pathogens refers to pathogens that are either closely related genetically or have a similar mechanism of pathogenicity to the pathogen of interest.
- Lower bound refers to the dose-response curve derived from pathogenesis studies of enteropathogenic *E. coli* (EPEC).
- Upper bound refers to the dose-response curve derived from pathogenesis studies of *Shigella dysenteriae*.

ESTIMATING THE RESPONSE

Estimating the number of symptomatic *E. coli* O157:H7 infections due to contaminated ground beef first requires an estimation of the total number of cases that occur annually in the United States from all causes.

Baseline Annual Number of *E. coli* O157:H7 Infections Due to All Causes

FoodNet surveillance data for 1996 to 1999 were used to estimate the annual baseline number of symptomatic *E. coli* O157:H7 infections (1999 is the most recent year for which a final report is available). For information about FoodNet, please see Chapter 2. For each year and FoodNet site, the number of cases per 100,000 population was calculated. This rate per 100,000 population was multiplied by that state's population and then divided by the total population of all sites, for that year, providing a weighted rate for each state. Weighted rates for each state were then summed, resulting in an annual incidence estimate for 1996 to 1999 of 1.53, 1.25, 1.95, and 2.09, respectively (Table 4-1).

TABLE 4-1 Population-Weighted Rate of Illness Caused by *E. coli* O157:H7

	Year			
	1999	1998	1997	1996
FoodNet State: California				
Cases reported to FoodNet[a]	23	35	19	22
FoodNet catchment population[a]	2,162,359	2,063,454	2,063,454	2,063,454
Unadjusted rate (per 100,000 person-years)	1.06	1.70	0.92	1.07
State population[b]	33,145,121	32,666,550	32,182,118	31,762,190
Weighted rate	0.47	1.07	0.58	0.67
State: Connecticut				
Cases	94	58	34	38
Catchment population	3,282,031	2,460,127	2,460,127	1,626,366
Unadjusted rate	2.86	2.36	1.38	2.34
State population	3,282,031	3,274,069	3,267,240	3,263,910
Weighted rate	0.12	0.15	0.09	0.15

(continued)

TABLE 4-1 (continued)

	Year			
	1999	1998	1997	1996
State: Georgia				
Cases	44	51	8	15
Catchment population	7,788,240	3,541,230	3,541,230	2,729,783
Unadjusted rate	0.56	1.44	0.23	0.55
State population	7,788,240	7,642,207	7,489,982	7,334,183
Weighted rate	0.06	0.21	0.03	0.08
State: Maryland[c]				
Cases	16	24		
Catchment population	2,450,566	2,444,280		
Unadjusted rate	0.65	0.98		
State population	5,171,634	5,130,072		
Weighted rate	0.04	0.07		
State: Minnesota				
Cases	175	209	199	239
Catchment population	4,775,508	4,725,419	4,687,408	4,657,758
Unadjusted rate	0.65	4.42	4.25	5.13
State population	5,171,634	4,725,419	4,687,408	4,648,081
Weighted rate	0.04	0.41	0.39	0.47
State: New York[c]				
Cases	94	22		
Catchment population	20,844,453	1,106,085		
Unadjusted rate	4.51	1.99		
State population	18,196,601	18,159,175		
Weighted rate	1.08	0.48		
FoodNet State: Oregon				
Cases	64	101	80	73
Catchment population	3,316,154	3,281,974	3,243,272	3,203,735
Unadjusted rate	1.93	3.08	2.47	2.28
State population	3,316,154	3,281,974	3,243,272	3,195,409
Weighted rate	0.08	0.20	0.16	0.14
TOTAL				
Cases	510	500	340	387
Catchment population	25,859,311	19,622,569	15,995,491	14,281,096
Unadjusted rate	1.97	2.55	2.13	2.71
States' population	75,675,289	74,879,466	50,870,020	50,203,773
Weighted rate	2.09	1.95	1.25	1.53

[a]Data obtained from FoodNet final reports for each calendar year from www.cdc.gov.

[b]State population estimates for July 1 of each calendar year from www.census.gov.

[c]Maryland and New York began surveillance in 1998.

To represent variability in the annual number of reported cases, these four weighted rates were placed into a discrete uniform probability distribution (DUniform [1.53, 1.25, 1.95, 2.09]). During Monte Carlo simulation, one of these four rates is selected at random with equal probability. The output of this simulation is a list of possible rates and the frequency at which each possible rate occurred during multiple iterations of the model. The median rate from this output was multiplied by the estimated 1999 U.S. population of 272.7 million (Table 4-3) to obtain an estimated baseline annual number of cases of symptomatic *E. coli* O157:H7 infection. The median baseline number of cases estimated by the model was 4,200 (3,500 and 5,700—2.5th and 97.5th percentiles, respectively). This estimated number of cases has been rounded to two significant digits.

Adjusting the Baseline for Underdiagnosis and Underreporting

The baseline annual number of *E. coli* O157:H7 cases was adjusted upward to account for recognized sources of underdiagnosis and underreporting. These sources include ill persons who do not seek medical care, physicians who do not obtain stool specimens from patients with *E. coli* O157:H7 infection, laboratories that do not culture all stool samples for *E. coli* O157:H7, and the ability to detect antigen in *E. coli* O157:H7-contaminated stool samples (test sensitivity). However, before making this upward adjustment, the baseline annual number of cases was divided into two groups—cases with bloody diarrhea and cases with nonbloody diarrhea—by multiplying the baseline number of cases by the proportion expected to have bloody diarrhea (Table 4-2). Cases were divided into these two groups because the likelihood of seeking medical care, obtaining a stool specimen, and testing a stool specimen for *E. coli* O157:H7 is greater for patients with bloody diarrhea than for those with nonbloody diarrhea.

A negative binomial distribution was then applied to each of the sources of underdiagnosis and underreporting described above, providing an estimation of the number of missed cases. This procedure was completed separately for each of the two pathways: patients with bloody diarrhea and patients with nonbloody diarrhea. The negative binomial probability distribution outputs the number of failures (i.e., unreported cases), given inputs of the number of successes (reported cases) and the probability of success (estimates derived from the literature, described below). The probability of success used in the negative binomial probability distribution was estimated using a beta probability distribution. The output of the beta probability distribution is the prevalence (proportion) of an event, given inputs of the number of successes, s, and the number of trials, n.

The median (most likely) number of cases generated by the negative binomial distribution was used as the number of "missed cases" for each source of underdiagnosis/underreporting. Beginning with the baseline annual number of cases (described above), the missed cases for each source are summed for each group (those with bloody diarrhea and those with nonbloody diarrhea), and then the two group totals are summed to give an estimate of the total annual number of cases of symptomatic *E. coli* O157:H7 infection in the United States.

The data used as inputs into the negative binomial distribution are described above and summarized in Table 4-2. The distributions are listed in Table 4-3. The Monte Carlo simulation methods used here produce a distribution of possible values for each of the outcomes. Table 4-4 and Figure 4-2 show the results of this process, including estimates of the annual number of cases with bloody and nonbloody diarrhea and the total annual number of cases for the United States. The 2.5th and 97.5th percentiles represent the uncertainty about the number of cases at each step. The number of cases shown has been rounded to two significant digits to avoid

TABLE 4-2 Sources of Data Used to Estimate the Number of Undetected Cases of *E. coli* O157:H7 Infection

Event	Data	Reference(s)
Cases with bloody diarrhea are reported	640 of 757 (84.5%) patients with *E. coli* O157:H7 had bloody diarrhea	Ostroff et al. 1989 Hedberg et al. 1997 Slutsker et al. 1997 Kassenborg et al. 2001
Ill persons seek medical care	88 of 1,100 (8.0%) survey respondents reported seeking medical care for diarrhea	CDC 1998
	37 of 76 (48.7%) *E. coli* O157:H7 cases with bloody diarrhea sought medical care	Cieslak et al. 1997 Hedberg et al. 1997
Physicians obtain culture from patients	699 of 1,943 (36.0%) physicians surveyed obtain cultures from patients presenting with nonbloody diarrhea; 1,515 of 1,943 (78.0%) physicians obtain cultures from patients presenting with bloody diarrhea	Hedberg et al. 1997
Laboratories culture stool samples for *E. coli* O157:H7	108 of 230 (47.0%) labs surveyed test nonbloody stool for *E. coli* O157:H7	CDC 1997
	182 of 230 (79.1%) labs test bloody stool for *E. coli* O157:H7	
Sorbitol MacConkey agar (SMAC) test sensitivity	0.75 = probability a sample test is positive given it is infected	Hedberg et al. 1997

overstating the precision of the model. Outputs for intermediate steps in the pathway (e.g., probability of seeking care, probability of having a stool sample taken) are not shown.

Data Used to Adjust for Underdiagnosis and Underreporting

The proportion of patients who had bloody diarrhea was derived from the literature. A total of 640 (84.5%) of 757 reported cases of *E. coli* O157:H7 infection presented with bloody diarrhea (Ostroff et al. 1989; Hedberg et al. 1997; Slutsker et al. 1997; Kassenborg et al. 2001). These data were used in a beta distribution with inputs of the number of successes, s=640 (i.e., persons with bloody diarrhea), and the total sample size, n=757 (number of cases of symptomatic *E. coli* O157:H7 infection) (see Tables 4-2 and 4-3).

Information on the proportion of ill persons seeking medical care, physicians who obtain stool samples from symptomatic patients, and laboratory testing practices was obtained from FoodNet surveys and is summarized in Table 4-2. A high percentage of persons with bloody diarrhea seek medical care. Cieslak et al. (1997) found that 32 (55.2%) of 58 cases with bloody diarrhea in an *E. coli* O157:H7 outbreak in Las Vegas reported seeking medical care. Data from this and another study (Hedberg et al. 1997) were input into a beta distribution with inputs of s=37 and n=76 to determine the most likely number of missed cases at this step and the associated uncertainty. In the Hedberg et al. (1997) study, 88 (8.0%) of 1,100 respondents who had nonbloody diarrhea reported seeking medical attention. These values were used in a beta distribution with s=88 and n=1,100 (Tables 4-2 and 4-3).

TABLE 4-3 Input Values and Distributions Used to Estimate the Annual Number of Cases of *E. coli* O157:H7 Infection with Bloody and Nonbloody Diarrhea and the Total Number of Cases in the United States

Epidemiologic Parameter	Distribution	
Population-weighted, reported rate of *E. coli* O157:H7 per 100,000 person-years, all FoodNet sites, 1996–99	Discrete Uniform (1.53, 1.25, 1.95, 2.09)[a]	
U.S. population (1999)	272.7 million	
P(Case with bloody diarrhea is reported)[b]	Beta (640 + 1, 757 – 640 + 1)[c]	
P(Case with nonbloody diarrhea is reported)	1 – Beta (640 + 1, 757 – 640 + 1)	
	Bloody	Nonbloody
P(Laboratory cultures stool sample for *E. coli* O157:H7)	Beta (182 + 1, 230 – 182 + 1)	Beta (108 + 1, 230 – 108 + 1)
P(Physician obtains culture from patient)	Beta (1,515 + 1, 1,943 – 1,515 + 1)	Beta (699 + 1, 1,943 – 699 + 1)
P(Ill person seeks medical care)	Beta (37 + 1, 76 – 37 + 1)	Beta (88 + 1, 1,100 – 88 + 1)

[a]In a discrete uniform distribution, each of the four values listed in parentheses is equally likely to be sampled during simulations.

[b]*P*=probability of the event described.

[c]The input format for a beta distribution is (s+1,n–s+1), where s=the number of events of interest and n=total number of events measured (e.g., the number of cases with bloody diarrhea [s] and the number of all cases of symptomatic *E. coli* O157:H7 infection [n]).

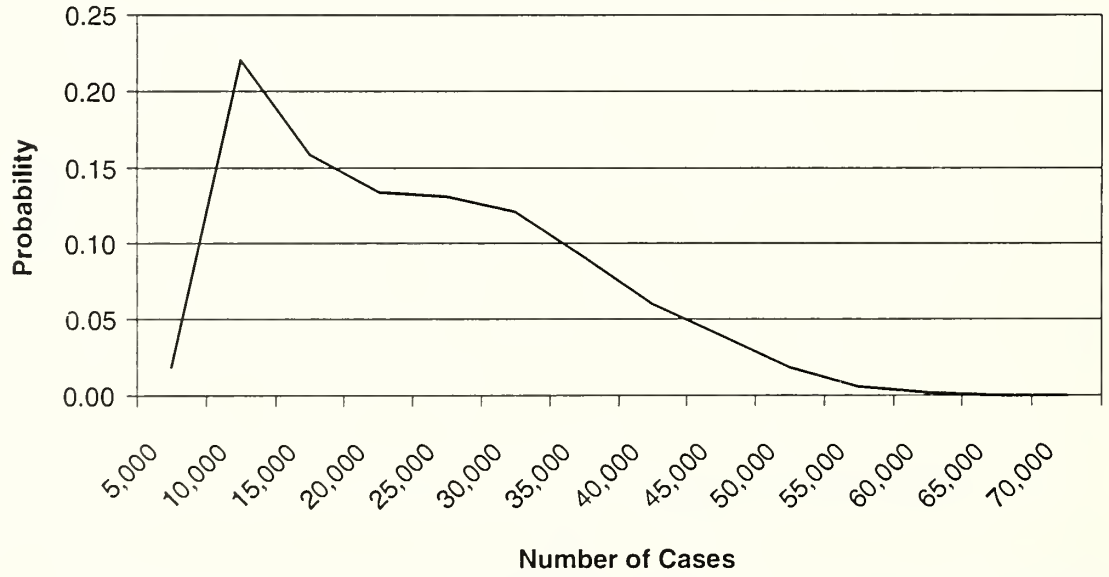

FIGURE 4-2 Estimated annual number of human cases of *E. coli* O157:H7 due to ground beef exposure.

TABLE 4-4 Number of Cases of Symptomatic *E. coli* O157:H7 Infection Due to All Exposures and Due to Exposure to Ground Beef Only (6,000 Iterations)

Number of Reported Cases	Median	2.5th and 97.5th Percentiles
All exposures		
Cases with bloody diarrhea	19,000	12,000 and 28,000
Cases with nonbloody diarrhea	74,000	45,000 and 116,000
Total annual cases	94,000	59,000 and 138,000
Ground beef exposures		
Cases with bloody diarrhea	3,800	1,000 and 9,000
Cases with nonbloody diarrhea	15,000	4,100 and 37,000
Total annual cases	19,000	5,300 and 45,000

Note: Number of cases has been rounded to two significant digits.

In a survey conducted in the FoodNet catchment area, 1,515 (78.0%) of 1,943 physicians reported that they obtained stool specimens from patients presenting with bloody diarrhea, and 699 (36.0%) of 1,943 physicians reported obtaining specimens from patients with nonbloody diarrhea (Hedberg et al. 1997). These data were fit to beta distributions (Tables 4-2 and 4-3).

In a national survey of clinical laboratories, 182 (79.1%) of 230 laboratories reported testing bloody stool for *E. coli* O157:H7 (CDC 1998), providing inputs for the beta distribution with s=182 and n=230 (Table 4-2). Only 108 (47.0%) of 230 laboratories reported testing all stool samples for *E. coli* O157:H7 (Hedberg et al. 1997), providing an s=108 and n=230 for input into a beta distribution (Tables 4-2 and 4-3). Hedberg et al. (1997) also reported that the sensitivity of the sorbitol MacConkey agar (SMAC) test used by the laboratories to identify *E. coli* O157:H7 in stool samples is 71% (Tables 4-2 and 4-3).

The model estimates that a median of 94,000 cases of symptomatic *E. coli* O157:H7 infection occur annually in the United States, accounting for underdiagnosis and underreporting (Table 4-4). Of these, an estimated 19,000 (20.2%) cases were characterized by bloody diarrhea. Mead et al. (1999) estimated that 73,480 cases of *E. coli* O157:H7 due to all exposures occur annually in the United States, approximately 20,000 fewer cases than the estimate derived by this risk assessment. This difference may be explained by differences in the methods used to derive the annual estimated number of cases. In the Mead et al. study, a weighted rate of 1.34 cases per 100,000 population was used to calculate a baseline number of cases. This rate is smaller than three of the four weighted rates used in this risk assessment (Table 4-1). In addition, Mead used a multiplier of 20 unreported cases for each reported case. In this risk assessment, unreported cases were estimated by several steps for two pathways: illnesses due to *E. coli* O157:H7 infection with bloody diarrhea and those with nonbloody diarrhea. This process resulted in 22 unreported cases for each reported case (94,000/4,200).

Estimating the Number of *E. coli* O157:H7 Illnesses Due to Contaminated Ground Beef (Etiologic Fraction)

To estimate the number of cases attributable to ground beef, the estimated total annual number of symptomatic *E. coli* O157:H7 infections for a given iteration was multiplied by an estimate of the proportion of cases due to exposure to ground beef (etiologic fraction). This calculation was done using Monte Carlo simulation and the inputs described below.

To estimate the etiologic fraction, data from studies of sporadic cases and outbreaks of *E.* coli O157:H7 were incorporated. Data from all outbreaks in which the route of transmission was identified were used, including those with waterborne and person-to-person transmission (CDC unpublished data). Two estimates were derived from outbreaks: the proportion of illnesses and the proportion of outbreaks due to ground beef exposure. During 1996 to 1999 (1999 is the most recent year for which data are available), ground beef was the most likely vehicle in 44 (30.1%) of 146 reported outbreaks of *E. coli* O157:H7 with an identified vehicle. This information was input into a beta distribution with s=44 and n=146. For the 146 outbreaks, 418 (11.1%) of 3,773 cases were attributed to ground beef; this information was input into a beta distribution with s=418 and n=3,773. Information from 48 outbreaks during 1996 to 1999 was excluded from this analysis.

Additional estimates of the etiologic fraction of illness due to ground beef contaminated with *E. coli* O157:H7 were obtained from four different case-control studies of mostly sporadic cases (MacDonald et al. 1988; Mead et al. 1997; Slutsker et al. 1998; Kassenborg et al. 2001). The etiologic fraction estimates for these studies were 17% (MacDonald et al. 1988), 26% (Mead et al. 1997), and 37% (Slutsker et al. 1998), and 7% and 8% for ground beef eaten away from home and at home, respectively (Kassenborg et al. 2001). The etiologic fractions of ground beef eaten at home or away from home were averaged to provide a single estimate.

These six estimates of the etiologic fraction, two from outbreak data and four from case-control studies, were input to a discrete distribution. Each of the six values were equally likely to be chosen during model simulation. During a given iteration, one of these six values was drawn at random. The etiologic fraction value drawn for a given iteration was multiplied by the estimated total number of cases for that iteration to arrive at the number of cases attributable to ground beef exposure. This process was repeated for the specified number of iterations during Monte Carlo simulation, producing a distribution of possible values for the annual number of cases attributable to ground beef.

Using the inputs described above, Monte Carlo modeling resulted in a median of 19,000 cases of symptomatic *E.* coli O157:H7 infection due to contaminated ground beef exposure (Table 4-4). However, uncertainty about the total number of cases implies that there may be fewer than 5,300 cases (2.5th percentile) or more than 45,000 cases (97.5th percentile) per year (Figure 4-2). This uncertainty distribution is used to develop the *E. coli* O157:H7 dose-response function. The median number of cases due to ground beef is 20.2% of the estimated median number of cases (94,000) due to all exposures.

DERIVING THE DOSE-RESPONSE FUNCTION FOR *E. COLI* O157:H7

The *E. coli* O157:H7 dose-response function was derived using information from three sources: (1) the estimated annual number of symptomatic *E. coli* O157:H7 infections due to ground beef exposure, (2) the estimated number of contaminated ground beef servings from the exposure assessment, and (3) the lower and upper bound dose-response curves derived using surrogate pathogens.

This section begins with a description of the beta-Poisson function used to fit dose-response data. followed by a description of how the lower and upper bound dose-response curves were developed from foodborne pathogens other than *E. coli* O157:H7 (surrogates). Then, the process for developing the dose-response function for *E. coli* O157:H7 in ground beef is described. The chapter ends with a discussion of the uncertainty about the estimated number of *E. coli* O157:H7 infections and contaminated servings.

Beta-Poisson Function

A beta-Poisson function was chosen to perform the dose-response analysis (Powell et al. 2000). This functional form assumes that a single organism is capable of infecting and inciting illness in an individual and that organisms operate independently within the host. Such assumptions are considered biologically plausible and defensible and can be used to derive a family of dose-response functions that include the beta-Poisson (WHO/FAO 2000; Buchanan et al. 2000; Haas et al. 1999).

Equation 4.1 is the beta-Poisson model, which predicts the probability of illness given a dose

$$p_i = 1 - (1 + d/\beta)^{-\alpha} \tag{4.1}$$

where

p_i = probability of illness,
α = alpha parameter,
d = dose of pathogen,
β = beta parameter = $N_{50}/(2\text{^}[1/\alpha] - 1)$, and
N_{50} = dose necessary to cause illness in 50% of those exposed.

The alpha and beta parameters needed in the beta-Poisson model are estimated by Equation 4.2, which is the maximum likelihood estimation routine developed by Regli et al. (1991). These estimates were obtained using the add-on program Solver, within Excel®. To briefly describe this process, Equation 4.2 is developed using an Excel spreadsheet, and the alpha and beta parameters are varied until Y is minimized. This process is performed separately for EPEC and *S. dysenteriae* data (described below):

$$\text{Y (minimized)} = 2\Sigma\{P_i * \ln(p_i/p_{oi}) + (T_i - P_i) * \ln[(1 - p_i)/(1 - p_{oi})]\} \tag{4.2}$$

P_i is the observed number of positive responses at the ith dose, p_{oi} is the observed proportion of response at the ith dose, T_i is the total number of subjects in the ith dose group, and p_i is the response estimated by the beta-Poisson function at the ith dose.

The output of these beta-Poisson models is the estimated proportion of persons expected to experience illness given a dose. The proportion of persons expected to fall ill at a given dose multiplied by the number of servings containing that dose, as estimated by the exposure assessment portion of the model, results in an estimate of the number of persons expected to become ill during a year.

Developing Upper and Lower Boundaries to the *E. coli* O157:H7 Dose-Response Function

No human clinical trial data are available for *E. coli* O157:H7, but they are available for a number of pathogens that can be used as surrogates (see Appendix B). These surrogates are used to form upper and lower boundaries between which the *E. coli* O157:H7 dose-response function is assumed to fit. This method is termed the envelope method because these upper and lower boundaries envelop the *E. coli* O157:H7 dose-response function (Vose 1996, p. 202). Therefore, the upper and lower boundaries describe the extent of uncertainty about the true *E. coli* O157:H7 dose-response.

Several *Shigella* and other *E. coli* species were considered as possible surrogates. In considering a species to use as a surrogate, a number of factors were evaluated, including availability of data, genetic relatedness, and similarities in transmission, infectivity, and pathogenicity. Other risk assessments of *E. coli* O157:H7 have used *Shigella* as a surrogate pathogen (Cassin et al. 1998; Marks et al. 1998).

E. coli O157:H7 may be most similar to *Shigella* spp. with regard to transmission and infectivity; however, *Shigella* spp. are invasive pathogens that multiply within host epithelial cells, whereas *E. coli* O157:H7 does not. Both are transmitted by food, although humans are the reservoir of *Shigella* spp. contamination of food and water. The probability of infection with low doses of *Shigella* spp. is thought to be high. There are four species of *Shigella* spp.: *S. sonnei*, *S. flexneri*, *S. boydii*, and *S. dysenteriae.* A clinical experiment in human volunteers has been conducted using *S. sonnei*; however, this trial used only one dose of pathogen. Without multiple data points in the form of administered dose levels, a curve cannot be fitted to generate parameters for the dose-response function; therefore, *S. sonnei* was not used as a surrogate. A substantial amount of human experimental data are available for one strain of *S. flexneri*; however, this organism does not produce Shiga toxins and thus was not chosen as a surrogate.

S. dysenteriae was selected as an upper bound to the *E. coli* O157:H7 dose-response function based on the assumption that *E. coli* O157:H7 is unlikely to be more pathogenic than this invasive *Shigella* species. Both *S. dysenteriae* type 1 and *E. coli* O157:H7 strains produce Shiga toxins, a virulence factor that appears to increase the severity but not necessarily the probability or frequency of illness. Similar to *E. coli* O157:H7, *S. dysenteriae* has a high probability of illness associated with low doses; both organisms cause hemolytic uremic syndrome (HUS).

The data for *S. dysenteriae* (Table 4-5) include dose groups of 4, 6, or 10 volunteers administered four-dose levels from 10 to 10,000 pathogen cells (Levine et al. 1973). These trials found a generally increasing proportion of symptomatic infection as the dose was increased, with 10% of persons exposed at the lowest doses and 83% of those exposed at the highest doses developing clinical symptoms.

Another surrogate, enteropathogenic *E. coli* (EPEC), was chosen to represent the lower bound of an *E. coli* O157:H7 dose-response function, based on the assumption that *E. coli* O157:H7 is unlikely to be less pathogenic than the EPEC. EPEC and *E. coli* O157:H7 have similar mechanisms of transmission, that is, by food, water, and person-to-person contact; however, unlike *E. coli* O157:H7, EPEC is principally a disease of children younger than 1 year of age and generally requires large doses (e.g., 100 million organisms) before a substantial probability of illness is observed. A substantial amount of data were available from human clinical trials for EPEC (Levine et al. 1978; Bieber et al. 1998). Therefore, three virulent EPEC strains were selected as surrogates. The data for EPECs (Table 4-6) include dose groups of two, four, five, or six volunteers administered six-dose levels from 10^6 to 10^{10} pathogen cells. In some trials, no one developed symptomatic infection at lower doses; all persons developed symptomatic infection at higher doses.

The dose and response information found in Tables 4-5 and 4-6 was used in Equations 4.1 and 4.2. Dose-response calculations were performed separately for each of the two surrogate organisms.

The estimated lower bound dose-response generated using EPEC clinical trial data and the estimated upper bound dose-response generated using *Shigella dysenteriae* data are illustrated in Figure 4-3. The estimated alpha and beta parameters are shown in Table 4-7.

TABLE 4-5 Data from Human Volunteers Administered Two Strains of *Shigella dysenteriae*

Shigella Dysenteriae Strain	Dose of Pathogen	Number of Persons Developing Symptoms	Total Persons Exposed	Proportion of Persons Developing Symptoms
M 131	10	1	10	0.10
A-1	200	1	4	0.25
M 131	200	2	4	0.50
M 131	2,000	7	10	0.70
A-1	10,000	2	6	0.33
M 131	10,000	5	6	0.83

Source: Levine et al. 1973.

TABLE 4-6 Data from Human Volunteers Administered Four Strains of Enteropathogenic *Escherichia coli* (EPEC)

EPEC Strain	Dose of Pathogen	Number of Persons Developing Symptoms	Total Persons Exposed	Proportion of Persons Developing Symptoms
O128	1,000,000	0	5	0.00
O127	1,000,000	0	4	0.00
O142	1,000,000	1	5	0.20
O128	100,000,000	0	5	0.00
O142	100,000,000	1	5	0.20
B-171-8	500,000,000	3	5	0.6
B-171-8	2,500,000,000	6	6	1
O128	10,000,000,000	0	5	0.00
O127	10,000,000,000	3	5	0.60
O142	10,000,000,000	5	5	1.00
B-171-8	20,000,000,000	2	2	1

Sources: Bieber et al. 1998; Levine et al. 1978.

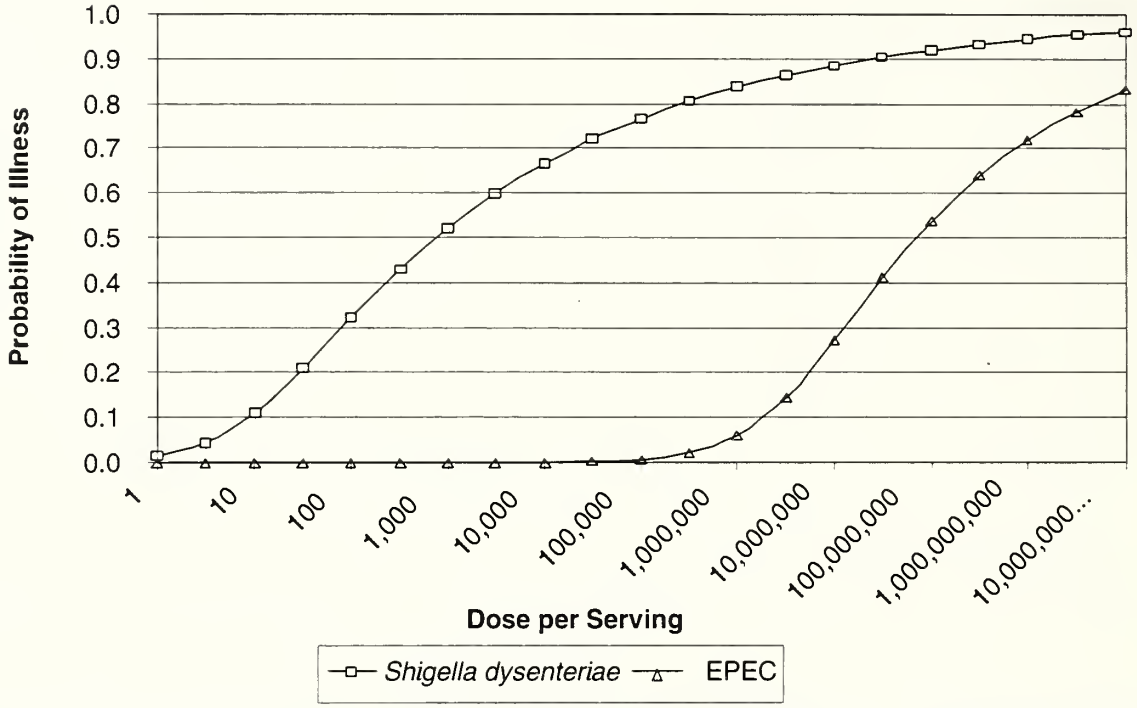

FIGURE 4-3 Dose-response curves for *Shigella dysenteriae* (Shig dys cumulative distribution function [cdf]) and enteropathogenic *E. coli* (EPEC cdf). The *Shigella dysenteriae* curve serves as the upper bound and EPEC as the lower bound to a dose-response curve for *E. coli* O157:H7.

TABLE 4-7 Alpha and Beta Parameters for the Upper and Lower Bound Beta-Poisson Models, *Shigella dysenteriae* and Enteropathogenic *Escherichia coli* (EPEC)

Surrogate Organism	Alpha	Beta
S. dysenteriae	0.157	9.17
EPEC	0.221	3,110,000

For the EPEC dose-response curve, the implied dose at which 50% of persons exposed will become ill (N_{50}) is 68 million organisms. *E. coli* O157:H7 is highly unlikely to have an N_{50} that is this high. For the *Shigella dysenteriae* dose-response curve, the N_{50} is 740 organisms. By using this pathogen to represent an upper bound, it is assumed that *E. coli* O157:H7 is unlikely to have an N_{50} lower than 740 organisms.

Process for Developing the *E. coli* O157:H7 Dose-Response Function

A beta-Poisson dose-response function for *E. coli* O157:H7 is derived from the distribution of *E. coli* O157:H7 illnesses attributable to ground beef (response) and the distribution of the number of *E. coli* O157:H7 organisms in consumed ground beef servings (dose) (Powell et al. 2000). The derived *E. coli* O157:H7 dose-response function is constrained to lie between beta-Poisson functions fit to *Shigella dysenteriae* and EPEC data. The derivation can be simply represented as

$$\text{Ex} \times \text{DR} = \text{TC} \qquad (4.3)$$

where Ex represents the exposure distribution, DR is the dose-response function, and TC is the total cases per year. If dose-response data for *E. coli* O157:H7 were available, a dose-response function could be fit to these data and Equation 4.3 could be directly solved for total cases. In the absence of dose and response data, available estimates for the total number of cases can be used with the model's estimates for the exposure distribution to determine the dose-response using Equation 4.3.

Uncertainty in Cases and Exposure Distribution

Uncertainty about the exposure distribution predicted by this model was illustrated as an output from Chapter 3. Uncertainty about the number of *E. coli* O157:H7 cases associated with ground beef was discussed above. These uncertainties are integrated in deriving the dose-response function for *E. coli* O157:H7 (Figure 4-4).

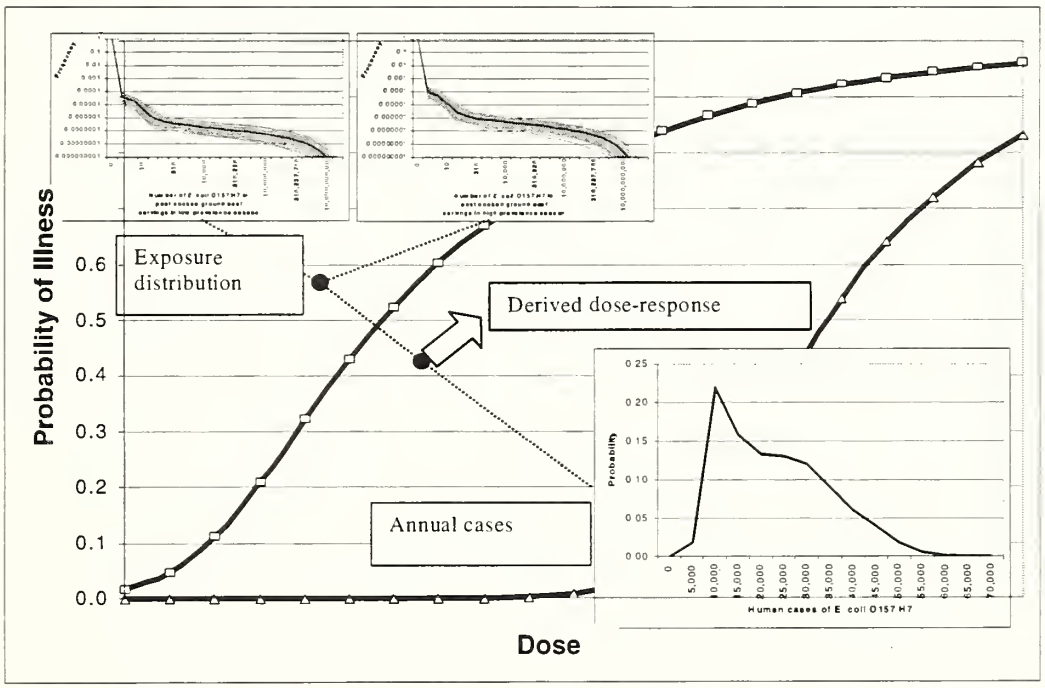

FIGURE 4-4 Illustration of process by which an *E. coli* O157:H7 dose-response function is derived from uncertain exposure distributions and uncertain total human cases.

Because the exposure assessment estimates exposure distributions for high and low prevalence seasons but the estimated total cases distribution reflects an annual number, the two seasonal exposure distributions must be combined to represent exposures in servings of ground beef across a full year. This annual exposure distribution is estimated by weighting each seasonal distribution by its number of months. Therefore, the high prevalence season is given a weight of $4 \div 12$ (for June through September) and the low prevalence season is given a weight of $8 \div 12$.

For a given draw from the uncertain exposure distributions and the total cases distribution, a best-fitting beta-Poisson function is determined by varying the alpha and beta parameters of that function. These parameters are constrained, however, by the lower and upper bound parameters estimated for *Shigella dysenteriae* and EPEC. The set of parameter values that result in predicting the specified total cases of *E. coli* O157:H7 illness given the exposure distribution is

saved, and the algorithm is repeated for another draw from the exposure and total cases distributions. With this method, the uncertainty regarding exposures and total cases per year is fully integrated into the estimate of a dose-response function.

Figure 4-5 shows the resulting uncertainty about the derived *E. coli* O157:H7 dose-response function. Each curve shows progressively higher percentiles of the derived dose-response function extending from the 5th to the 95th percentiles. The median dose-response function in this range is assumed to be the best estimate.

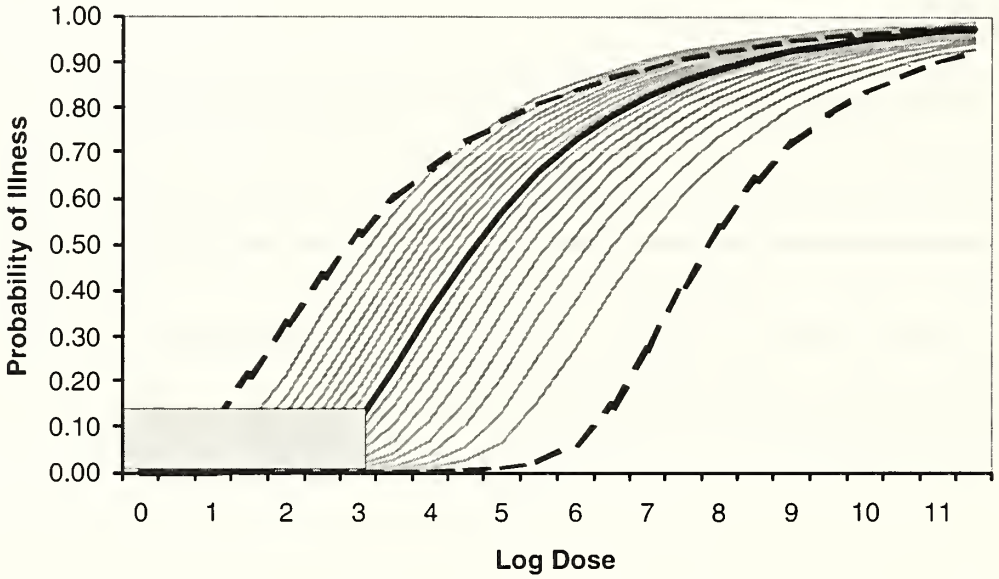

FIGURE 4-5 Derived dose-response curves from combining output of hazard characterization and exposure assessment. Curves represent percentiles of uncertainty distribution (ranging from 5th to 95th percentile) about the *E. coli* O157:H7 dose-response function. The thick line is the median dose-response curve. The dashed lines are boundary dose-response functions fit to *Shigella dysenteriae* and enteropathogenic *E. coli* (EPEC). The rectangle in the lower left represents the combined range of uncertainty of the dose and response derived from the 1994 outbreak in the northwestern United States. Source: Bell et al. 1994.

Uncertainty about the *E. coli* O157:H7 dose-response function extends almost across the full range enveloped by the lower and upper bound curves. Nevertheless, this uncertainty suggests more confidence in dose-response functions that lie closer to the *Shigella dysenteriae* boundary than in those that lie closer to the EPEC boundary. Therefore, the results of this derivation suggest that the dose-response function for *E. coli* O157:H7 more closely approximates that estimated for *Shigella dysenteriae* than for EPEC.

The derived dose-response function for *E. coli* O157:H7 also shows consistency with information obtained from a ground beef-associated outbreak in the northwestern United States. Uncertainty about the average exposure dose and attack rate in this outbreak is shown in Figure 4-5. The majority of the percentiles for the derived dose-response function fit within the outbreak's uncertainty range. However, even the boundary formed by the *Shigella dysenteriae* dose-response function fails to explain all of the outbreak's uncertainty.

Effect of Uncertainty in Exposures and Cases

Although the derivation of the *E. coli* O157:H7 dose-response function includes the uncertainty from the exposure assessment and the total number of cases occurring per year, it does not suggest the relative contribution of each source of uncertainty to the overall uncertainty in the dose-response function. To examine this relative effect, the exposure distribution and the total cases were considered fixed, in turn, and the uncertainty about the other was used to derive the dose-response function.

Figure 4-6 shows dose-response functions estimated by setting the exposure distribution at its median but using the 5th and 95th percentiles from the total cases per year distribution. The N_{50} for the dose-response curve fit to the 5th percentile of cases is about 3.5 logs. In other words, the dose-response function predicts that 50% of those exposed to an average dose of 3.5 logs of *E. coli* O157:H7 will become ill. The N_{50} for the dose-response curve fit to the 95th percentile of cases is about 6.5 logs. This range in uncertainty is slightly less than the range shown in Figure 4-5. It is also reasonably symmetrical about the median curve shown in Figure 4-5.

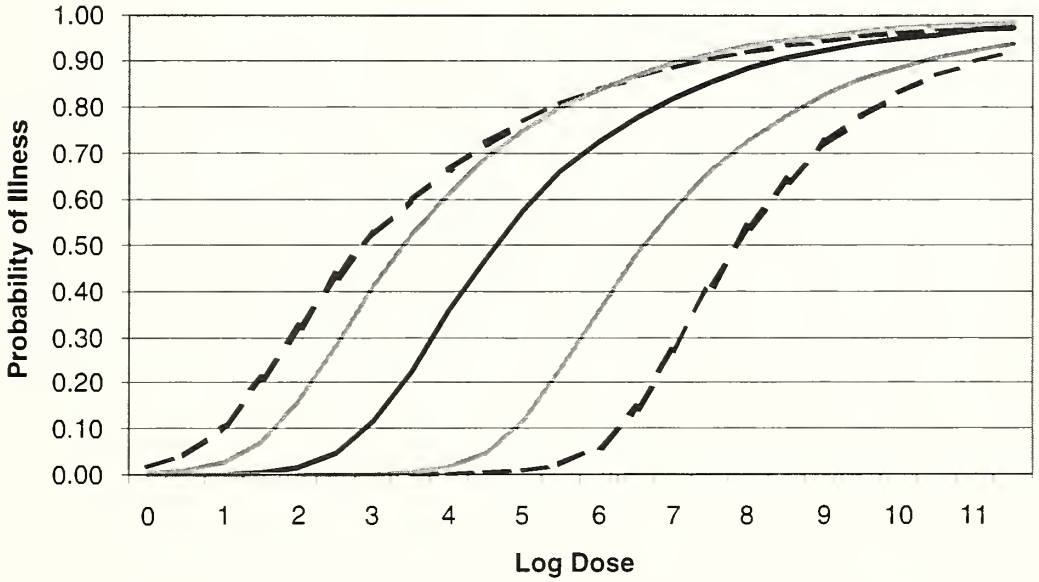

FIGURE 4-6 Dose-response curves that result from setting exposure distribution at the median and using 5th and 95th percentiles (grey lines) of cases predicted from hazard characterization. The solid dark line is the median dose-response function including uncertainty about exposures and cases (Figure 4-5). The dashed lines are boundary dose-response functions fit to *Shigella dysenteriae* and enteropathogenic *E. coli* (EPEC).

Figure 4-7 shows dose-response functions estimated by setting the total number of cases at the median but using the 5th and 95th percentiles from the exposure distribution. This figure is generally similar to Figure 4-6. In Figure 4-7, the N_{50} for the dose-response curve fit to the 5th percentile of the exposure distribution is about 3 logs. The N_{50} for the dose-response curve fit to the 95th percentile of the exposure distribution is about 6 logs. This range is shifted to the left relative to the range shown for Figure 4-6. This shift implies that fixing the number of cases at its median value would move estimated dose-response functions closer to the *Shigella dysenteriae* curve than fixing the exposure distribution at its median (as done in Figure 4-6).

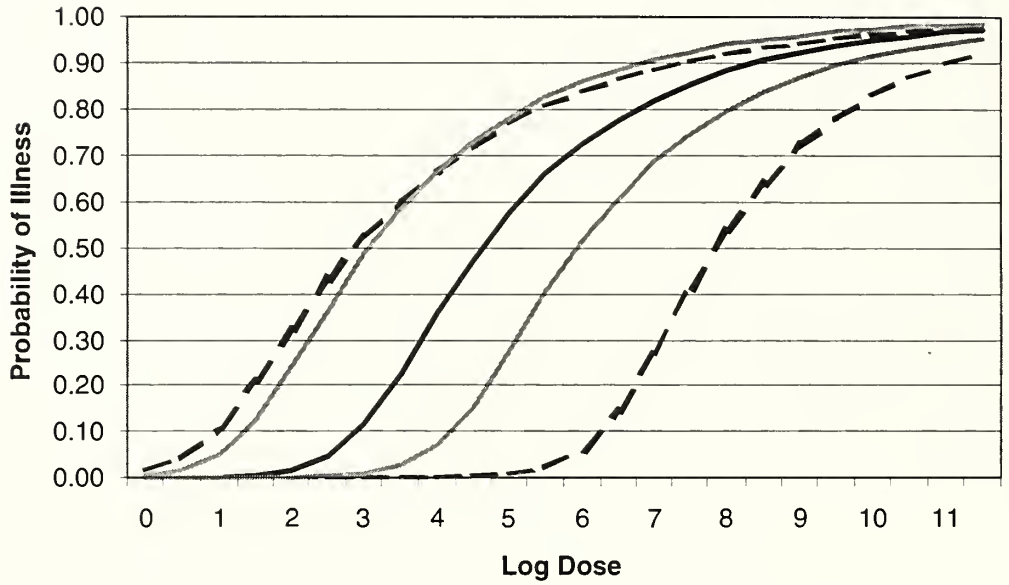

FIGURE 4-7 Dose-response curves that result from setting total *E. coli* O157:H7 cases per year at the median and using 5th and 95th percentiles (grey lines) of the exposure distribution predicted from the exposure assessment. The solid dark line is the median dose-response function including uncertainty about exposures and cases (Figure 4-5). The dashed lines are boundary dose-response functions fit to *Shigella dysenteriae* and enteropathogenic *E. coli* (EPEC).

The implication of this analysis is that neither uncertainty about the exposure distribution nor uncertainty about the total number of cases dominates the uncertainty about the *E. coli* O157:H7 dose-response function. Instead, both sources of uncertainty contribute equally to the overall uncertainty.

ESTIMATING SEVERE CLINICAL OUTCOMES DUE TO *E. COLI* O157:H7 INFECTION

The estimates generated by this portion of the model are not used in developing a dose-response curve for *E. coli* O157:H7. Instead, they describe the consequences of symptomatic infection. Given the lack of dose-response data, the probability of various clinical outcomes is assumed to be independent of the dose of *E. coli* O157:H7 consumed. Estimating the clinical outcomes of symptomatic infection is essential for future cost-benefit analyses of intervention options. Estimates are provided for severe illnesses due to ground beef exposure and due to all exposures.

The number of persons who experienced hospitalization, HUS, thrombotic thrombocytopenic purpura (TTP), or death was estimated using data from 203 outbreaks that occurred between 1982 and 1998 (CDC unpublished data). A total of 4,478 cases occurred during the 203 outbreaks; of these, 968 (21.6%) cases resulted in hospitalization, 228 (5.1%) cases progressed to HUS or TTP, and 28 (0.6%) cases resulted in death (Table 4-5). Only summary data were available for these outbreaks, preventing calculation of conditional probabilities. Therefore, for the purposes of modeling, it is assumed that HUS or TTP cases occur only among hospitalized patients and that deaths occur only among those patients with HUS or TTP. The data from these outbreaks were used as inputs to beta distributions and simulated.

The data inputs estimating the number of hospitalizations were s=968 and n=4,478; the number of cases with HUS or TTP, s=228 and n=968; and the number of deaths, s=28 and n=228. Recall that s is the number of events of interest and n is the total number observed. Applying these proportions to all cases assumes that pathogenicity is similar among strains of *E. coli* O157:H7 and that outcome is independent of dose.

The median annual estimated number of patients with bloody diarrhea who sought medical care was 9,400 (Table 4-8); of these, 2,000 (21.3%) persons were hospitalized. Of the hospitalized patients, the model estimates that a median of 460 (23.0%) patients developed HUS or TTP and that 50 (10.9%) of these patients died. These estimates are similar to the estimated 2,168 hospitalizations and 52 deaths annually due to *E. coli* O157:H7 infection reported by Mead et al. (1999).

The proportion of cases with severe clinical outcomes attributable to ground beef exposure is also presented in Table 4-8. The model estimates that a median of 1,800 severe cases (patients with bloody diarrhea who sought medical care) are due to ground beef exposure annually. Of these 1,800 cases, the model estimates that 400 (22.2%) will be hospitalized and that, of these, 90 (22.5%) will develop HUS or TTP and 10 (11.1%) HUS/TTP patients will die.

TABLE 4-8 Number of Severe Outcomes Due to *E. coli* O157:H7 Infection and the Distributions and Inputs Used to Calculate These Outcomes (6,000 Iterations)

Parameter	Distribution	
Proportion of cases hospitalized	Beta (968 + 1, 4,478 – 968 + 1)[a]	
Proportion of hospitalized cases progressing to HUS/TTP	Beta (228 + 1, 968 – 228 + 1)	
Proportion of HUS/TTP cases resulting in death	Beta (28 + 1, 228 – 28 + 1)	
Severe Health Outcomes	**Median**	**2.5th and 97.5th Percentiles**
All exposures		
Severe (patient with bloody diarrhea, seeks medical care)	9,400	6,300 and 12,000
Hospitalized	2,000	1,300 and 2,600
HUS/TTP	460	300 and 630
Deaths	50	30 and 100
Ground beef exposures		
Severe (patient with bloody diarrhea, seeks medical care)	1,800	1,000 and 4,100
Hospitalized	400	100 and 900
HUS/TTP	90	30 and 210
Deaths	10	1 and 30

Note: Number of cases has been rounded to two significant digits (one significant digit for numbers less than 100). HUS = hemolytic uremic syndrome; TTP = thrombotic thrombocytopenic purpura.

[a]The input format for a beta distribution is (s+1,n–s+1), where s=the number of events of interest and n=total number of events measured (e.g., the number of cases with bloody diarrhea [s] and the number of all cases of symptomatic *E. coli* O157:H7 infection [n]).

SENSITIVE SUBPOPULATIONS

Certain age groups have a higher reported incidence of *E. coli* O157:H7 infection. Surveillance from FoodNet sites in 1999 shows that 1- to 9-year-olds had the highest incidence among all age groups (Figure 4-8, CDC 2000). Nationwide in 1998, 1- to 4-year-olds had the highest incidence, at 4.57 reported cases per 100,000 population (CDC 1999). Young children also appear to be more susceptible to developing HUS (see Chapter 2).

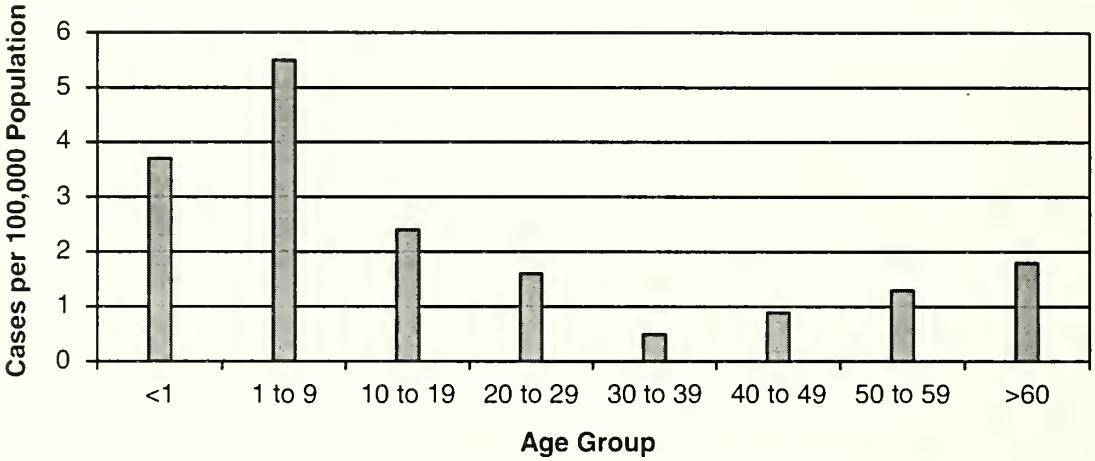

FIGURE 4-8 Number of reported cases of *E. coli* O157:H7 infection due to all routes of transmission, by age group, FoodNet sites, 1999.

The reason why children have the highest reported incidence of *E. coli* O157:H7 infection is not known. Relative to adults, children may be more likely to receive medical care during an episode of diarrhea or bloody diarrhea and be more likely to be tested for *E. coli* O157:H7. They may also have better access to health care, a higher likelihood of being reported to public health officials, more opportunities for exposure, increased susceptibility to infection, or some combination of all of these factors. Children are more likely than adults to develop HUS as a sequela of infection with *E. coli* O157:H7. Kidney damage that occurs during HUS is a result of Shiga toxin binding to specific receptors present on kidney cells. These receptors appear to be present in the kidneys of children but not adults (Lingwood et al. 1998).

Given that children consistently have the highest rate of *E. coli* O157:H7 infection relative to older age groups, it would seem reasonable to conduct a separate dose-response analysis of children. However, data on the proportion of *E. coli* O157:H7 infections due to ground beef, by age, are scarce. Also, the epidemiology of *E. coli* O157:H7 in children is complex, as described above. It is not known whether the high incidence in children is due to more children having the disease relative to adults or to artifacts of the health care and public health reporting systems, and little or no data are available to answer these questions. Therefore, this risk assessment does *not* include a separate dose-response analysis for children.

VALIDATION OF THE *E. COLI* O157:H7 DOSE-RESPONSE FUNCTION USING OUTBREAK DATA

An epidemiologic investigation traced a 1992 to 1993 outbreak of *E. coli* O157:H7 to consumption of hamburgers at a chain of fast-food restaurants (Chain A) in the Pacific

Northwest (Bell et al. 1994). Data from this investigation were used to develop a separate dose-response function to validate the dose-response function derived separately in this risk assessment. The data were not used directly in this risk assessment because the contamination levels of *E. coli* O157:H7 in the ground beef servings were not directly correlated with the severity of illness (i.e., the number of *E. coli* O157:H7 organisms consumed by each human case was not known).

A total of 501 culture-confirmed cases were documented to occur during this outbreak, including 398 (79.4%) primary cases, 48 (9.6%) secondary cases, and 55 (11.0%) cases that could not be classified as either primary or secondary. Of the 398 patients with primary disease in Washington state, 374 (93.9%) had eaten at Chain A in the previous 10 days. A total of 344 (92.0%) of 374 primary cases who ate at Chain A reported eating a regular (45-gram) hamburger. The median age of cases was 8 years, ranging from 4 months to 88 years. Forty-five (9.0%) patients developed HUS and 3 died of complications of HUS. The median age of HUS patients was 5 years, ranging from 1 to 68 years.

In response to the outbreak, approximately 255,000 45-gram hamburger patties were recalled from Chain A restaurants in Washington (Bell et al. 1994). These patties had been produced on November 19, 1992, at a processing plant in California. The recalled patties represented 43% of all regular hamburgers produced for Chain A at the California plant on that day, for a total production of 593,023 patties. The processing plant had sent 62% of that day's production (367,673 patties) to Washington. Therefore, the number of hamburger patties sold and consumed was equal to the number sent to Washington minus the number recalled (367,673 – 255,000 patties), or 112,673 patties.

The number of *E. coli* O157:H7 organisms per serving that occurred during this outbreak was quantified in six raw ground beef samples from implicated lots (Marks et al. 1998). The samples were enumerated for *E. coli* O157:H7 by the most probable number (MPN) method and were found to contain 0.3, 0.9, 1.5, 2.8, 4.3, and 15 colony-forming units per gram (CFU/g), respectively (Johnson et al. 1995; Tuttle et al. 1999). The distribution for the concentration of *E. coli* O157:H7 in the raw ground beef, d, was modeled by assuming that the quantity

$$\{[\ln(d)] - m\}/[s(1/n)^{1/2}] \sim t_{n-1}$$

is distributed as a t-distribution with $n-1$ degrees of freedom, where m is the mean of the $n=6$ log densities and s is the standard deviation of the log densities. Multiplying the distribution for d (CFU/g) by a serving size of 45 grams yields an estimated median per serving load of 96 CFU of *E. coli* O157:H7 before cooking (90% confidence interval, 5 to 1,844 CFU). This estimate is similar to the findings of Tuttle et al. (1999), who calculated a median of 67.5 organisms per raw ground beef patty (range, 13.5 to 675 organisms per patty).

To determine the effect of cooking on the final number of *E. coli* O157:H7 organisms, Bell et al. (1994) reported cooking 16 regular hamburgers according to Chain A's routine practices. After the frozen patties were cooked for 1 minute on each side on a 191°F grill, all of them had at least one internal temperature measurement below 68.3°C (155.0°F) (range, 41.7 to 81.1°C [107.1 to 177.98°F]). Ten had a measurement below 60.0°C (140°F). The minimum internal cooking temperature was modeled as a custom cumulative distribution with a minimum value of 37.8°C (100°F), a 6.25th percentile of 41.7°C (107.1°F), a 62.5th percentile of 60.0°C (140.0°F), and a maximum of 68.3°C (155.0°F).

Based on a study by Juneja et al. (1997), Marks et al. (1998) predicted the log reduction of *E. coli* O157:H7 in hamburgers due to cooking to be

$$\log_{10}(N_f/N_0) = 13.93 - 0.12*T$$

where N_0 is the number of organisms before cooking, N_f is the number of organisms after cooking, and T is cooking temperature (°F). Combining the distributions for the number of organisms in a raw patty prior to cooking with the cooking temperatures described above, this equation suggests that cooking rendered 50% of the hamburger patties free of *E. coli* O157:H7. From the estimate described above, 112,674 patties were purchased at Chain A restaurants; therefore, half of these, or 56,337 patties, were estimated to still be contaminated after cooking. The simulated distribution for the amount of viable *E. coli* O157:H7 per serving that remained after cooking has a median value of 23 CFU per serving (1 and 926 CFU per serving, 2.5th and 97.5th percentiles, respectively). This simulated estimated number of organisms is in agreement with a study of 76 recalled ground beef patties from this outbreak (Tuttle et al. 1999), where the median most probable number of organisms was determined to be 67.5 per uncooked patty (range, 13.5 to 675).

At this ingested dose, the uncertainty about the attack rate is estimated using a beta distribution. Inputs to this distribution were the number of primary cases (374) that had eaten at Chain A in the 10 days prior to illness, adjusted for underdiagnosis and underreporting (the input, *s*), and the number of patties contaminated with at least one *E. coli* O157:H7 organism after cooking (n=56,337). To adjust for underdiagnosis and underreporting, the number of primary cases that had eaten at Chain A was multiplied by a factor of 1 to 20 using a uniform probability distribution. A uniform distribution randomly chooses a value in the specified range during a given iteration. Therefore, 374 was multiplied by the randomly drawn value between 1 and 20 during each iteration of the model, resulting in a list of the possible number of actual cases that had occurred during the outbreak.

Modeling the underreporting factor in this manner accounts for uncertainty in the degree of underreporting that had occurred during this outbreak. A factor of 1 indicates no underreporting occurred; a factor of 20 indicates that 20 cases occurred for each reported case and is the underreporting factor used in Mead et al. (1999) for *E. coli* O157:H7. Because of the extensive publicity about this outbreak, the degree of underreporting is likely to be somewhat less than the estimated national average of 20.

A Monte Carlo simulation of 100,000 iterations resulted in a median value of 70 cases per 1,000 contaminated servings consumed (10 and 130 cases per 1,000 servings, 2.5th and 97.5th percentiles, respectively) at a median of 23 CFU per serving. For the outbreak, the probability of illness given a dose is consistent with the *E. coli* O157:H7 dose-response curve in Figure 4-5. In this figure, the outbreak information is represented by the rectangle in the lower left corner of the graph.

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5

Risk Characterization

In this chapter, the risk characterization integrates the results of the exposure assessment (Chapter 3) with the results of the hazard characterization (Chapter 4) to estimate the risk of illness from *E. coli* O157:H7 in ground beef. The exposure assessment describes the probability of exposure to various doses of *E. coli* O157:H7 (e.g., number of *E. coli* O157:H7 organisms per ground beef serving). The hazard characterization derived a dose-response function to describe the probability of illness for these various doses. Characterization of the risk of illness from *E. coli* O157:H7 in ground beef is considered from several perspectives based on the following:

- Level of risk: individual, community, and population;
- Duration of exposure: per serving, per annum, and lifetime risk; and
- Population variability of risk: by season, age, or location.

This risk characterization also includes an analysis to identify factors (model inputs) that influence the occurrence and extent of *E. coli* O157:H7 contamination in combo bins, grinder loads, and ground beef servings and the subsequent risk of illness (model outputs). This type of analysis is generally referred to as a sensitivity analysis. Two types of sensitivity analyses are used in this risk assessment: (1) correlation analysis and (2) dependency analysis.

DEFINITION OF KEY TERMS

The following key terms are used throughout this chapter:

- Risk is the probability of the occurrence of an adverse outcome (e.g., illness or death) resulting from exposure to a hazard. In this risk assessment, risk refers to the probability of illness (number and severity) resulting from consuming a single ground beef serving contaminated with a specific number of *E. coli* O157:H7 organisms.
- Scope of the risk estimate refers to whether we are considering the risk of illness for an individual, a community, or an entire population.

- "Typical" individual risk refers to the probability of illness for an individual consuming a single serving of ground beef. In this risk characterization, the "typical" individual is defined as someone who purchases ground beef that is contaminated at the median concentration and stores and cooks that product in a way that is consistent with the median of the growth and cooking distributions (Table 5-1). This type of analysis does not apply to specific individuals.
- Community risk refers to the probability of illness for an entire community under a given exposure scenario. In this risk characterization, the risk is illustrated for a community exposed to a single grinder load contaminated with *E. coli* O157:H7.
- Population risk refers to the probability of illness from *E. coli* O157:H7 in ground beef across the U.S. population. This type of risk estimate is useful for guiding food safety policy decision making.
- Duration of exposure refers to the length of time (e.g., per serving, per annum, or lifetime) for which a risk estimate was assessed.
- Risk per serving refers to the risk of *E. coli* O157:H7 illness from consuming a single serving of ground beef.
- Risk per annum refers to the risk of *E. coli* O157:H7 illness from consuming ground beef over the course of a year.
- Lifetime risk refers to the risk of *E. coli* O157:H7 illness from consuming ground beef over the course of a lifetime.
- Dose is the number of *E. coli* O157:H7 organisms in a single serving of ground beef.
- Population risk by season, age, and location refers to the stratified characterization of the risk of illness from *E. coli* O157:H7 in ground beef to provide further insight regarding the public health risks to specific subpopulations (e.g., based on seasonal exposure, age, and consumption patterns).
- Factors are model inputs that influence the prevalence and number of *E. coli* O157:H7 in ground beef or, more generally, influence the overall risk of *E. coli* O157:H7-related illness from ground beef. These model inputs may include one or more of the following: production practices, time and temperature controls during processing, storage and handling practices for ground beef during retail and preparation, or how thoroughly a ground beef serving was cooked.
- Sensitivity analysis refers to the quantitative process of identifying factors (model inputs) in the farm-to-table continuum that contribute to the occurrence of *E. coli* O157:H7 in ground beef or the subsequent risk of illness.
- Correlation analysis is one type of sensitivity analysis used to identify uncertain factors (model inputs) that influence either the occurrence of *E. coli* O157:H7 in ground beef or the subsequent risk of illness (model outputs). This type of sensitivity analysis identifies important factors quickly but only works for those that are uncertain.
- Dependency analysis is another type of sensitivity analysis used to identify factors (model inputs) that influence either the occurrence of *E. coli* O157:H7 in ground beef or the subsequent risk of illness (model outputs). This type of sensitivity analysis is resource intensive but identifies both uncertain and certain factors (model inputs) in the risk assessment model.

RISK OF ILLNESS FROM *E. COLI* O157:H7

The estimated risk of illness from *E. coli* O157:H7 in ground beef varies depending on the level at which the risk estimate is focused—that is, whether one considers the risk of illness for an individual consuming a single serving of ground beef; a community of individuals experiencing similar exposures to *E. coli* O157:H7 in ground beef that came, for example, from the same grinder load; or the risk of illness across the entire U.S. population. The estimated risk of *E. coli* O157:H7 illness also varies depending on the duration of exposure—that is, whether one considers the risk of illness on a per serving, per annum, or lifetime basis. To characterize the risk of illness from *E. coli* O157:H7 in ground beef, it is important to clearly define the type of risk estimate under consideration (e.g., individual lifetime risk of illness versus a population per annum risk of illness). The type of risk estimate developed depends on the problem under consideration for which the risk assessment was developed: to estimate the median health risk to individuals, better understand an outbreak scenario, or develop food safety policy. Several types of risk estimates are considered below.

Risk of Illness for an Individual

A "typical" individual's risk of *E. coli* O157:H7 illness from ground beef can be calculated from point estimates taken from output distributions in the exposure assessment combined with the median (50th percentile) *E. coli* O157:H7 dose-response curve (Table 5-1). Using this approach, a "typical" individual's probability of being exposed to a single *E. coli* O157:H7 organism in ground beef is somewhere between 1 in 1,500 (6.9×10^{-4}) and 1 in 1 million (9.2×10^{-7}).[1] Using the median dose-response curve for *E. coli* O157:H7, this equates to a lifetime risk of *E. coli* O157:H7 illness from ground beef for the "typical" individual that is between 1 in 8 million [$(6.9 \times 10^{-4})(1.7 \times 10^{-4}) = 1.17 \times 10^{-7}$] and 1 in 6 billion [$(9.2 \times 10^{-7})(1.7 \times 10^{-4}) = 1.56 \times 10^{-10}$].[2] Using similar calculations, the annual "typical" individual's risk of *E. coli* O157:H7 illness from ground beef is somewhere between 1 in 600 million and 1 in 400 billion.

This illustration is for the "typical" individual; it assumes that an individual always purchases the median product and always stores and cooks ground beef in accordance with the median of the population. If such an individual were typical of all individuals in the United States, the risk of *E. coli* O157:H7 would be extremely small for the entire population. Such an individual does not, of course, actually exist. The risk of illness for a specific individual from a specific serving of ground beef depends on when and where the ground beef was produced, how it was stored and handled, and how it was cooked. It also depends on the consumption patterns of the specific individual—how much (serving size) and how often (frequency) a specific individual consumes ground beef. Moreover, a specific individual may be more or less susceptible to illness or severe consequences of illness if exposed to *E. coli* O157:H7 in ground beef than predicted using the median dose-response curve. Consequently, a specific individual's risk of *E. coli* O157:H7

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[1] A "typical" individual's probability of consuming ground beef with at least 1 *E. coli* O157:H7 organism is calculated as follows: $10^{(\log[\text{number of contaminated ground beef servings purchased over a lifetime}) + \log(\text{number of organisms per contaminated serving}) + (\text{change in the number of } E.\ coli \text{ O157:H7 organisms in a serving of ground beef from storage conditions}) + (\text{decrease in the number of } E.\ coli \text{ O157:H7 organisms in ground beef from cooking})]}$. The data used in this calculation are presented in Table 5-1.

[2] This is calculated based on multiplying the probability of exposure to a particular number of *E. coli* O157:H7 organisms in a ground beef serving (dose) by the probability of illness (response) given this exposure (dose) (Table 5-1).

TABLE 5-1. Data from the Exposure Assessment (Chapter 3) and Hazard Characterization (Chapter 4) Are Used to Estimate the Risk of *E. coli* O157:H7 Illness for a "Typical" Individual

Information Used to Estimate the Risk of *E. coli* O157:H7 Illness for a "Typical" Individual	
1. General Information	
• U.S. population:	260 million
• Annual number of ground beef servings:	18.2 billion (Tables 3-24, 3-25, and 3-26)
2. Typical Individual	
• Average lifetime:	70 years
• Average serving size of ground beef:	87 grams (Tables 3-24, 3-25, and 3-26)
• Average number of ground beef servings purchased annually:	70 servings (18.2 billion servings/260 million people; Tables 3-24, 3-25, and 3-26)
3. *E. coli* O157:H7 Contamination in Uncooked Ground Beef Servings	
• Probability of a contaminated ground beef serving:	0.2% to 0.5% (5th and 95th percentiles) (Figure 3-27 and Equation 3-40)
• Typical level of contamination per serving:	1 to 3 *E. coli* O157:H7 organisms (5th and 95th percentiles) (Figure 3-27 and Equation 3-40)
• Typical number of contaminated servings purchased in a lifetime:	9 to 23 servings
4. Typical Growth and Decline in the Number of *E. coli* O157:H7 during Storage, Handling, and Cooking	
• Increase in the number of *E. coli* O157:H7 during storage and handling conditions:	0 logs (Figure 3-23)
• Decrease in the number of *E. coli* O157:H7 from freezing:	1 log (Table 3-18)
• Decrease in the number of *E. coli* O157:H7 from cooking:	5 to 6 logs (Figure 3-20)
5. Dose-Response Curve (median)	Figure 4-6

illness may be very different from a "typical" individual's risk of *E. coli* O157:H7 illness. Characterization of risk of *E. coli* O157:H7 illness for the "typical" individual, however, is useful in understanding that the overall risk is low. However, specific individuals may be at greater or lower risk of *E. coli* O157:H7 illness because of differences in consumer and retail behavior practices (storage, handling, and preparation conditions for ground beef); susceptibility to illness; or changes in production, slaughter, or retail practices that lead to either more contaminated ground beef servings (increased prevalence) or a greater number of *E. coli* O157:H7 organisms in contaminated ground beef servings. Some of these influence variables will be considered in the "Population Risk by Season, Age, and Location" section.

Risk of Illness for a Community—Simulated Outbreak

Characterizing the risk of *E. coli* O157:H7 illness from ground beef for a community is useful in evaluating the likelihood of a foodborne outbreak and the factors that would contribute to such an outbreak. As an example, consider a community exposed to a large amount of *E. coli* O157:H7-contaminated ground beef from a single grinder load that is stored and cooked under the same conditions (e.g., it was purchased, handled, and prepared by a single retail establishment).

This *E. coli* O157:H7 risk assessment indicates that grinder loads of ground beef can have concentrations of *E. coli* O157:H7 as high as 1 organism per 100 grams.[3] Given an average serving size of 87 grams,[4] nearly all servings of ground beef generated from such a grinder load would contain at least 1 *E. coli* O157:H7 organism. This risk assessment predicts growth of *E. coli* O157:H7 in ground beef in only 1% to 2% of storage scenarios (Figure 3-23), and only about 1 in 1,000 ground beef servings will have *E. coli* O157:H7 organisms grow to a level of 5.5 logs. Nevertheless, if all of the ground beef servings generated from the grinder load in this example were stored (e.g., refrigerated) in a manner that allowed growth of *E. coli* O157:H7, then each ground beef serving could contain a substantial number of *E. coli* O157:H7 organisms prior to cooking.[5] If all of these ground beef servings were undercooked, reducing the number of *E. coli* O157:H7 organisms in each ground beef serving by only 3 logs,[6] then each ground beef serving for consumption would be expected to contain about 270 *E. coli* O157:H7 organisms.[7] If individuals consume only one serving of *E. coli* O157:H7-contaminated ground beef, then about 3,200 people would be expected to become ill from *E. coli* O157:H7.[8] On the other hand, if all of these ground beef servings had been subjected to similar cooking conditions that resulted in a decrease of 5.5 logs,[9] only 12 people would be expected to become ill from *E. coli* O157:H7.

This example illustrates how an outbreak might develop in a community. It is not difficult to imagine that a single grinder load might be distributed to a single community. In fact, local commercial preparers of ground beef might receive, store, and cook volumes of ground beef consisting of entire grinder loads. A similar scenario occurred in the northwestern U.S. outbreak described in Chapter 4 (Tuttle et al. 1999; Bell et al. 1994). While such outbreaks are uncommon, sporadic illness often results from individual ground beef servings following "high risk" scenarios (e.g., improper storage, handling during processing, distribution, retail and preparation, or undercooking of ground beef servings). Characterizing the per serving risk of *E.*

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[3]The *E. coli* O157:H7 risk assessment predicts that ground beef servings from grinder loads containing more than 1 *E. coli* O157:H7 organism have a 0.0116% probability of occurring.

[4]Calculated as the weighted average of the amount of ground beef (in grams) consumed by an individual for each age category. See Tables 3-24, 3-25, and 3-26.

[5]About 5.5 logs of *E. coli* O157:H7 in each ground beef serving.

[6]The *E. coli* O157:H7 risk assessment predicts that 3 logs or less occurs 25% of the time.

[7]This is calculated from Equation 3-42: $DOSE_{pop} = BACT_{pop} + Growth_{pop} - LR_{pop}$, where the number of *E. coli* O157:H7 organisms per ground beef serving (dose) is equal to the number of *E. coli* O157:H7 in an uncooked ground beef serving (multiplied by the number of servings) plus the increase in the number of *E. coli* O157:H7 organisms during storage and handling minus the decrease in *E. coli* O157:H7 organisms as a result of cooking. In this scenario, $DOSE_{pop} = BACT_{pop} + Growth_{pop} - LR_{pop} = \log_{10}(0.01 \times 87) + 5.5 - 3 = 2.44$ logs in each cooked ground beef serving (= 275 *E. coli* O157:H7 organisms in each cooked ground beef serving).

[8]Calculated by using the dose-response equation (Equation 4-3) for ground beef servings containing 270 *E. coli* O157:H7 organisms and multiplying by the total number of ground beef servings from this grinder load (78,000 servings).

[9]The *E. coli* O157:H7 risk assessment predicts that this level of cooking (e.g., resulting in a 5.5 log reduction in *E. coli* O157:H7 organisms in each ground beef serving) is the median of the cooking distribution.

coli O157:H7 illness from ground beef within a community is useful for evaluating the conditions that are likely to lead to a foodborne outbreak.

Risk of Illness for the U.S. Population

The annual risk of *E. coli* O157:H7 illness from ground beef within the U.S. population can be estimated by considering the entire exposure assessment distribution (e.g., the probability of consuming *E. coli* O157:H7 in ground beef for all possible doses). When the median exposure distribution and the median dose-response function are used, the risk of illness at each exposure dose can be calculated as the product of these two distributions (Table 5-2).

TABLE 5-2 Risk of Illness for U.S. Population Using Median Exposure and Dose-Response Distributions

Log of *E. coli* O157:H7 per Serving	Number of *E. coli* O157:H7 per Serving	Probability of Exposure (Ex)	Probability of Illness Given Exposure (DR)	Risk of Illness (Ex × DR)
0.0	1	5.5×10^{-05}	1.7×10^{-04}	9.5×10^{-09}
0.5	3	2.9×10^{-05}	5.5×10^{-04}	1.6×10^{-08}
1.0	10	6.1×10^{-06}	1.7×10^{-03}	1.0×10^{-08}
1.5	32	1.2×10^{-06}	5.4×10^{-03}	6.5×10^{-09}
2.0	100	7.7×10^{-07}	1.6×10^{-02}	1.3×10^{-08}
2.5	316	5.3×10^{-07}	4.7×10^{-02}	2.5×10^{-08}
3.0	1,000	4.3×10^{-07}	1.2×10^{-01}	5.0×10^{-08}
3.5	3,162	3.4×10^{-07}	2.3×10^{-01}	7.7×10^{-08}
4.0	10,000	2.7×10^{-07}	3.6×10^{-01}	9.7×10^{-08}
4.5	31,623	2.2×10^{-07}	4.8×10^{-01}	1.1×10^{-07}
5.0	100,000	1.8×10^{-07}	5.8×10^{-01}	1.0×10^{-07}
5.5	316,228	1.5×10^{-07}	6.6×10^{-01}	1.0×10^{-07}
6.0	1,000,000	1.2×10^{-07}	7.3×10^{-01}	8.9×10^{-08}
6.5	3,162,278	9.7×10^{-08}	7.8×10^{-01}	7.6×10^{-08}
7.0	10,000,000	7.4×10^{-08}	8.2×10^{-01}	6.1×10^{-08}
7.5	31,622,777	5.4×10^{-08}	8.6×10^{-01}	4.6×10^{-08}
8.0	100,000,000	3.8×10^{-08}	8.9×10^{-01}	3.4×10^{-08}
8.5	316,227,766	2.5×10^{-08}	9.1×10^{-01}	2.3×10^{-08}
9.0	1,000,000,000	1.4×10^{-08}	9.3×10^{-01}	1.3×10^{-08}
9.5	3,162,277,660	4.8×10^{-09}	9.4×10^{-01}	4.5×10^{-09}
10.0	10,000,000,000	8.5×10^{-10}	9.5×10^{-01}	8.1×10^{-10}
10.5	31,622,776,602	5.5×10^{-11}	9.6×10^{-01}	5.3×10^{-11}
11.0	100,000,000,000	2.0×10^{-12}	9.7×10^{-01}	1.9×10^{-12}
Population risk of illness from *E. coli* O157:H7 per serving				9.6×10^{-07}

Table 5-2 shows this population risk to be nearly 1 illness in each 1 million (9.6×10^{-7}) servings of ground beef consumed annually. At each half-log dose interval, the risk of becoming ill depends on the probability of being exposed to that dose and the probability of illness given that dose. When the entire exposure distribution is considered, the sum of the risk of illness across all doses represents the population risk. This annual U.S. population risk estimate is based on the central tendencies (median) of both the exposure distribution and dose-response functions.[10]

This risk of illness, 9.6×10^{-7} illnesses per serving, is comparable to the findings of Cassin et al. (1998) and Marks et al. (1998). Cassin et al. (1998) conducted a quantitative risk assessment of *E. coli* O157:H7 in ground beef hamburgers cooked at home, for Canada, and calculated a mean per serving risk of illness of 5.1×10^{-5} for adults and 3.7×10^{-5} for children. The probability of illness generated by another risk assessment of *E. coli* O157:H7 in ground beef in the United States ranged from 3×10^{-4} to 7×10^{-8} (Marks et al. 1998). The risk of illness predicted from this risk assessment ranges from 3.3×10^{-7} to 2×10^{-6} per serving (median, 9.6×10^{-7}) (Table 5-2).

Given approximately 18.2 billion servings of ground beef consumed per year, the risk assessment predicts about 17,500 cases of *E. coli* O157:H7 illness per year (50th percentile). The median number of cases per year predicted from public health surveillance data in the hazard characterization is approximately 19,000. Because the uncertainty distributions describing the exposure distribution (e.g., the probability of an *E. coli* O157:H7 dose in a ground beef serving) and dose-response function (e.g., the probability of illness given a dose of *E. coli* O157:H7 in a ground beef serving) are not symmetrical, these two estimates of illness do not precisely correspond (i.e., the median of the product of these two random variables does not equal the product of their respective median values because these distributions are asymmetric).

Risk of Severe E. coli O157:H7 Illness

Given this population risk of *E. coli* O157:H7 illness from ground beef, the probability of severe illnesses can be estimated. As noted in Chapter 4, about 20% of all cases develop bloody diarrhea and 49% of these cases seek medical attention. Of those persons who develop bloody diarrhea and seek medical attention, about 21.6% are severe enough to be hospitalized. Of these hospitalized cases, about 24% are hemolytic uremic syndrome (HUS) cases and about 12% of those cases result in death. The population risk of being hospitalized but recovering is 2.0×10^{-8}, the population risk of developing HUS but recovering is 4.2×10^{-9}, and the population risk of death is 5.9×10^{-10} per ground beef serving. These outcomes of *E. coli* O157:H7 illness, which represent the severest forms of this disease for humans, occur very infrequently on a "per serving" basis. If 18.2 billion servings of ground beef are consumed per year, these population risks imply that, on an "per annum" basis, 370 people are hospitalized but recover, 87 people develop HUS but recover, and 11 people die as a result of *E. coli* O157:H7-contaminated ground beef.

Risk of E. coli O157:H7 Illness as a Function of Exposure (Dose)

The risk of human illness from *E. coli* O157:H7 in ground beef is the result of two divergent trends:

[10]Uncertainty about this risk ranges from about 1 illness in every 3 million consumed ground beef servings at the 5th percentile to about 2 illnesses in every 1 million consumed ground beef servings at the 95th percentile.

1. Consumers are more likely to be exposed to a lower rather than a higher number of *E. coli* O157:H7 organisms (dose) in a ground beef serving (Figure 3-29; Table 5-2); and
2. Consumers are more likely to become ill when exposed to a higher rather than a lower number of *E. coli* O157:H7 organisms (dose) (Figure 4-7; Table 5-2).

These divergent trends are observed in Table 5-2, which shows that increasing dose (e.g., number of *E. coli* O157:H7 organisms) is associated with decreasing probability of exposure and increasing probability of illness. Therefore, the change in risk of illness as dose increases is dependent on the rate at which exposure probability is declining and the dose-response probability is increasing. Figure 5-1 uses the information in Table 5-2 to show how the risk of illness from *E. coli* O157:H7 changes as dose changes.

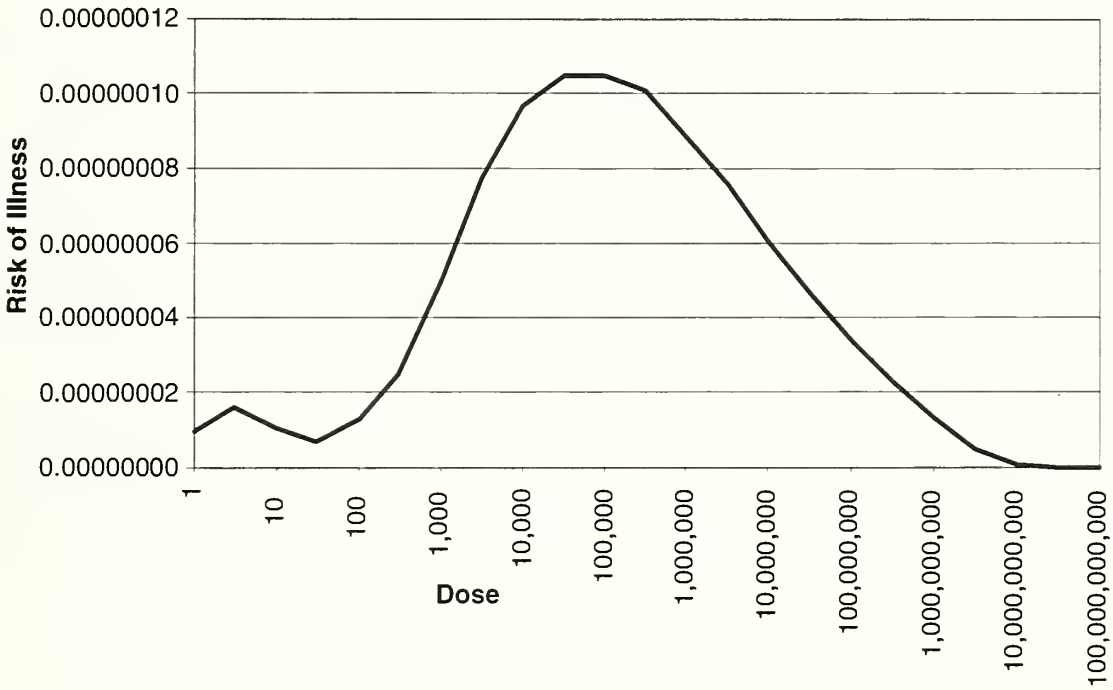

FIGURE 5-1 Risk of illness for U.S. population by dose.

Figure 5-1 shows that the highest risk of illness is associated with doses around 100,000 *E. coli* O157:H7 organisms per serving. Although the probability of exposure is greatest at a dose of 1 organism per ground beef serving (5.5×10^{-05}), the dose-response function predicts a very low probability of human illness given an exposure of just 1 *E. coli* O157:H7 organism (1.7×10^{-04}). This results in a low risk of illness ($5.5 \times 10^{-05} \times 1.7 \times 10^{-04} = 9.5 \times 10^{-09}$). At a dose of 100,000 organisms per ground beef serving, however, the probability of exposure is much lower (1.8×10^{-07}), but the probability of illness is much higher (0.58). Consequently, the risk of illness from exposure to 100,000 *E. coli* O157:H7 organisms ($1.8 \times 10^{-07} \times 0.58 = 1.0 \times 10^{-07}$) is higher than from exposure to 1 *E. coli* O157:H7 organism.

One interpretation of Figure 5-1 is that reducing the number of *E. coli* O157:H7-contaminated ground beef servings, but not the number of *E. coli* O157:H7 organisms in a ground beef serving, would lower the risk of illness at each dose level (i.e., decrease the amplitude of the curve). Such a reduction might occur by improved controls in the slaughter process that result in fewer contaminated ground beef servings. Alternatively, improved storage and/or cooking behavior by consumers and food preparers would decrease the number of *E. coli*

O157:H7 organisms in contaminated ground beef servings but not change the total number of contaminated servings (i.e., shift the curve to the left but leave the amplitude unchanged). Either reducing the number of *E. coli* O157:H7-contaminated ground beef servings or the number of *E. coli* O157:H7 organisms in contaminated ground beef servings would result in a reduction in the number of *E. coli* O157:H7 illnesses occurring per year.

Figure 5-1 indicates that reducing the number of *E. coli* O157:H7-contaminated servings actually results in a greater reduction in risk relative to reducing the number of *E. coli* O157:H7 in contaminated ground beef servings. A tenfold reduction in the number of *E. coli* O157:H7-contaminated ground beef servings results in a population risk of 9.6×10^{-08} per serving. A tenfold reduction in the number of *E. coli* O157:H7 organisms in contaminated ground beef servings results in a population risk of 5.5×10^{-07} per serving. This suggests that interventions focused on reducing the prevalence of *E. coli* O157:H7 (e.g., improved controls during slaughter and processing) are more effective at reducing the risk of illness than those focused on reducing the number of *E. coli* O157:H7 in consumed ground beef servings (i.e., storage and cooking conditions). However, this analysis does not suggest which intervention, if either, is more feasible to achieve.

The preceding discussion illustrates that a population estimate of risk is the sum of the risks faced by all individuals in the population. Therefore, the population risk estimate should be interpreted as a summary measure of risk that can be used for policy analysis or comparison with other risk estimates. The population risk is not indicative of the risk for any one individual. In other words, it is incorrect to assume that, given a population risk of 1 illness in every 1 million servings, each serving a person consumes has this risk of illness. Individual consumer risk is not necessarily random. The risk of illness from a serving of ground beef for a specific consumer can depend on when and where the ground beef was produced, how it was stored, and how the serving was cooked. The specific consumer may also be more susceptible to illness or severe consequences of illness if exposed. These factors are not necessarily controllable by the individual, but they are also not necessarily randomly occurring. The next sections consider the influence of such factors on the risk of illness from *E. coli* O157:H7 in ground beef.

POPULATION RISK BY SEASON, AGE, AND LOCATION

The risk of illness from *E. coli* O157:H7 in ground beef can vary among U.S. subpopulations based on differences in exposure (by seasonal contamination or behavioral differences) or host susceptibility (by age). Characterization of the risk of illness from *E. coli* O157:H7-contaminated ground beef can be used to target intervention strategies and risk communication messages. This risk assessment considers the risk of illness by seasonal exposure, age of the consumer, and location of the meal.

Variability in the Risk of Illness by Season

Variability in seasonal exposure may influence the risk of illness from *E. coli* O157:H7 in ground beef. The exposure assessment predicts that consumers are exposed to more *E. coli* O157:H7-contaminated ground beef servings during the "high prevalence season" (June to September) than during the "low prevalence season" (October to May) (see Chapter 3). This seasonal trend in exposure to *E. coli* O157:H7 in ground beef may be associated with the increased number and severity of *E. coli* O157:H7 cases reported during June through September (see Chapter 2).

The risk of illness is substantially greater in the high prevalence season at all doses relative to the low prevalence season. Figure 5-2 compares the risk of illness between the low and high prevalence seasons using the median exposure distribution for each season and the median dose-response function. For a dose of *E. coli* O157:H7 in ground beef servings ranging from 1 to 10 logs, each curve shows the product of the probability of exposure to that dose and the probability of illness given that dose. Both high and low prevalence seasons have similar shaped distribution curves for illness and are consistent with the shape shown in Figure 5-1. This indicates that the risk of illness from *E. coli* O157:H7 in ground beef servings follows the same trend over the same dose range.

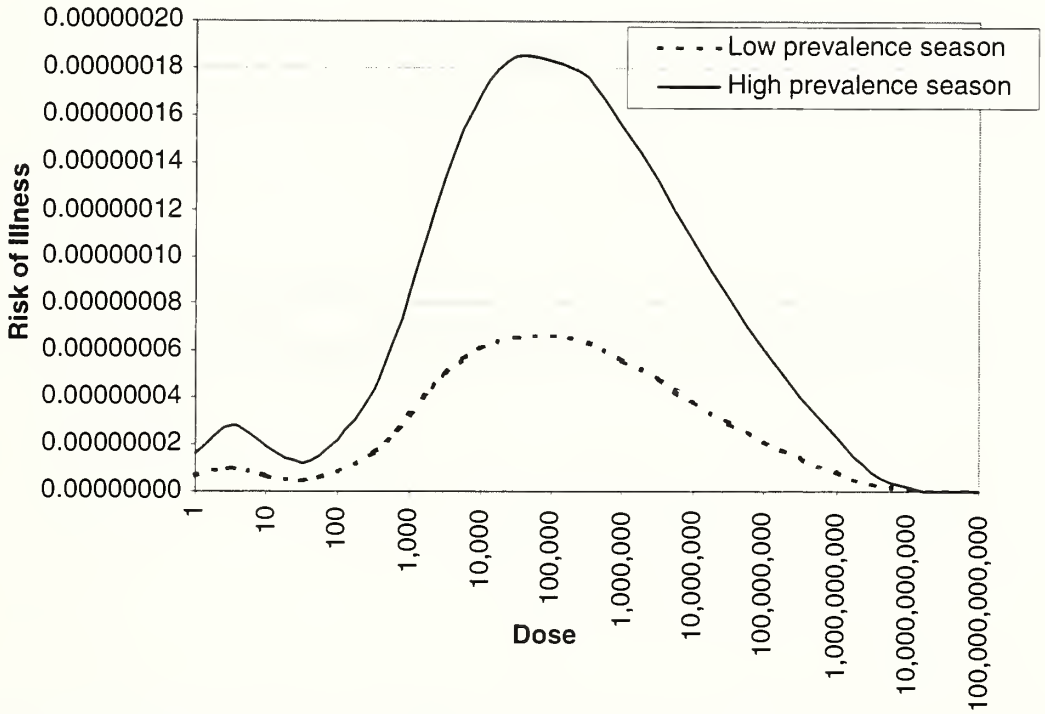

FIGURE 5-2 Risk of illness for U.S. population by dose for low and high prevalence seasons.

The only influence of season in this risk assessment occurs because live cattle, carcasses, and ground beef are more contaminated in the high prevalence season (June to September). No data were available on possible seasonal differences in consumer or retail storage and preparation of ground beef meals (e.g., grilled hamburgers in July versus baked meat loaf in November). Similarly, no data were available on seasonal consumption patterns for ground beef. Seasonal consumption data would provide information on how much ground beef was consumed and in what form (e.g., ground beef patty, meat loaf, or meatballs) during June to September versus other months of the year.[11] As a result, the similar shape of the two curves in Figure 5-2 simply reflects the assumption of similar consumer behavior practices (storage and cooking) for both high and low prevalence seasons.

[11]The type of ground beef meal consumed is important because ground beef meals are handled and cooked differently (e.g., ground beef patties consumed on the Fourth of July may have more time-temperature abuse at a picnic and are more likely to be undercooked on a grill than meat loaf consumed in January that may have been baked in the oven).

The greater prevalence of contaminated ground beef servings in the high prevalence season is reflected in the greater risk of illness across all doses. When the risk of illness is summed across all doses, the population risk of illness is 1.7×10^{-6} in the high prevalence season and 6.0×10^{-7} in the low prevalence season. Therefore, about 1 in every 600,000 servings consumed during the high prevalence season is predicted to result in illness, while about 1 in every 1.6 million servings consumed in the low prevalence season results in illness. These differences imply that risk of illness is about three times greater in the high prevalence season than in the low prevalence season.

The hypothetical linkage between live cattle, ground beef, and human *E. coli* O157:H7 illnesses is strongly supported by these seasonal findings. Of the 18.2 billion ground beef servings consumed annually, it is assumed that one-third are consumed during the high prevalence season and two-thirds are consumed during the remainder of the year. Combining this consumption pattern information with the seasonal risk per ground beef serving estimates implies that 58% of illnesses occur during the high prevalence season, while 42% occur during the low prevalence season. This finding is consistent with FoodNet data that show 64% of illnesses occur during June through September. Such consistency is noteworthy because the model only accounts for seasonality in live cattle and grinder loads of ground beef. Therefore, without any adjustment for seasonal differences in ground beef storage or cooking, these results imply that seasonal changes in prevalence on the farm subsequently influence levels of *E. coli* O157:H7 in combo bins, grinders loads, and servings and predict changes in illnesses in a manner consistent with human health surveillance data. Furthermore, these results suggest that variability in consumer behaviors may contribute to an increased number of *E. coli* O157:H7 illnesses observed in the summer months. Further research on consumer and retail behaviors is needed to validate the assumption that improper storage and cooking practices (e.g., time and temperature abuses) for ground beef are more likely during the summer months.

Variability in the Risk of Illness by Age of the Consumer

Age of the consumer has been identified as a risk factor for illness from *E. coli* O157:H7 in ground beef. In hazard characterization (Chapter 4), a higher apparent incidence of *E. coli* O157:H7 illnesses was reported for 1- to 9-year-olds. Other data suggest that most of the elevated risk occurs in children 0 to 5 years old (Mead et al. 1999).

The exposure assessment was used to generate an exposure distribution for children 0 to 5 years old and persons 6 years and older (Figure 5-3). The exposure distribution for 0- to 5-year-olds is shifted slightly to the left, reflecting a smaller average ground beef serving size (44 grams) compared with the average serving size for all other ages (90 grams). Because of the smaller serving size, children under 5 years old are less likely to be exposed to *E. coli* O157:H7 organisms in ground beef (i.e., they have a lower probability of consuming an *E. coli* O157:H7-contaminated ground beef serving and, if a contaminated serving is consumed, it is likely to have a lower number of *E. coli* O157:H7 organisms).

Although children 0 to 5 years old are less likely than older persons to be exposed to *E. coli* O157:H7 in ground beef, they are disproportionately represented among all reported *E. coli* O157:H7 cases. If young children are less exposed to *E. coli* O157:H7 in ground beef but more likely to become ill from *E. coli* O157:H7, then they may be (1) more susceptible to illness from the exposures they experience, (2) more likely to be diagnosed by a physician than other age

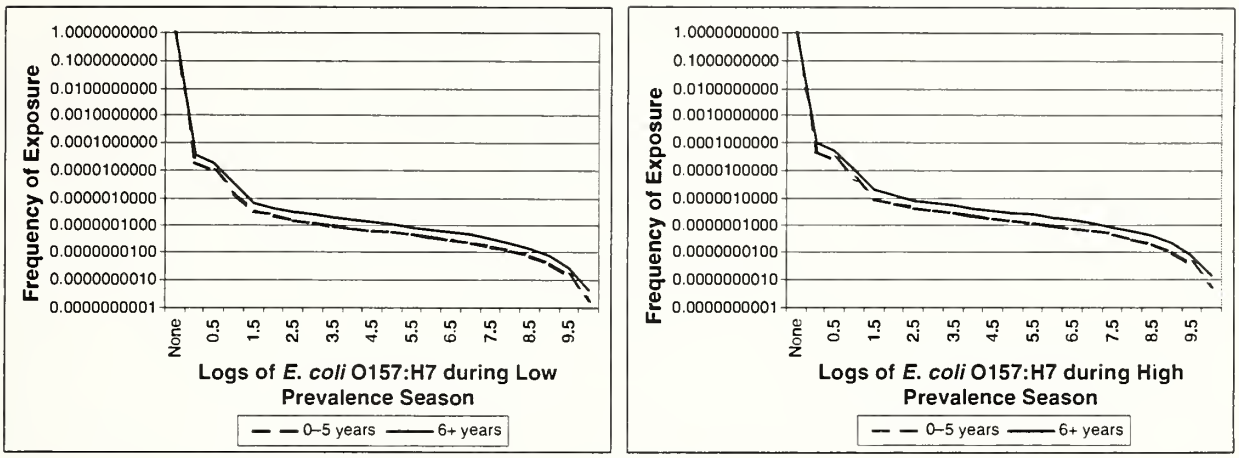

FIGURE 5-3 Comparison of predicted seasonal exposure distributions for children 0 to 5 years old versus people 6 years and older.

groups, or (3) more exposed to other sources of *E. coli* O157:H7 (e.g., daycare, petting farm, swimming pool) than the remainder of the population.[12]

If children ages 0 to 5 are more susceptible to illness from *E. coli* O157:H7, then a more sensitive dose-response curve than that derived for the general population should be used. Nevertheless, no data are available to estimate a different dose-response function for young children. If the upper bound *E. coli* O157:H7 dose-response curve derived from *Shigella dysenteriae* surrogates is used, then the risk of illness for children 0- to –5-years-old is estimated to be 2.4×10^{-6} per ground beef serving. This is comparable to estimates by Cassin et al. (1998) for the average (mean) risk of illness for children of 3.7×10^{-5} per ground beef serving. If young children are more susceptible to illness from *E. coli* O157:H7-contaminated ground beef, then their risk may be up to 2.5 times greater than that of the general U.S. population (2.4×10^{-6} versus 9.6×10^{-7}). Children 0- to 5-years-old consume only about 7% of all ground beef servings, but a more susceptible dose-response curve implies that about 15% of all illnesses occur in this age category.

Young children may be more susceptible to illness when exposed to *E. coli* O157:H7, but the available data do not rule out the possibility that reported illnesses for children are affected by various surveillance biases. For example, it is possible that the etiologic fraction of *E. coli* O157:H7 cases attributed to ground beef for young children may be lower than that reported for the general population. For instance, young children are exposed to *E. coli* O157:H7 via child-care facilities. This route of exposure may be important for this age group and would reduce the etiologic fraction of cases attributed to ground beef. Furthermore, adjustments to reported cases used for the general population may overestimate the proportion of cases in young children. It seems likely that young children are more likely than older persons to see a health care worker when they are sick. For example, young children are also more likely to develop HUS, and such a severe illness certainly requires medical attention. Based on the available data, however, the existence and magnitude of these biases cannot be ascertained.

[12]Exposure to other sources of *E. coli* O157:H7 may confound the etiologic fraction of *E. coli* O157:H7 cases attributable to ground beef (Chapter 4).

Variability in the Risk of Illness by Location of Meal

As more meals are consumed outside the home in the United States, there is a growing interest in the relative risk of foodborne illness from eating at home versus "away from home" (HRI). The 1994–1996, 1998 Continuing Survey of Food Intakes by Individuals indicates that 65% of ground beef meals are consumed outside the home (e.g., Tables 3-24, 3-25, and 3-26). While this risk assessment includes data on where ground beef meals were consumed, data on variability in food preparation behavior between consumers (home) and food preparers (HRI) are lacking. These data are needed to estimate the amount of *E. coli* O157:H7 contamination (dose) in ground beef servings prepared at home and at HRI. While it is plausible that HRI preparation practices for ground beef are more stringent under the Food Code (FDA 1999), data are needed to support such an assumption. Storage and cooking time and temperature data are available for ground beef meals cooked at home (Audits International 1999). When HRI storage and cooking time and temperature data become available, the risk of illness from home-prepared and HRI-prepared ground beef servings can be compared. The effects of consumer storage and cooking practices on the risk of *E. coli* O157:H7 illness from ground beef will be further evaluated in the context of sensitivity analysis.

Other Population Risk Variability

As more data become available, a more detailed picture of the risk of illness from *E. coli* O157:H7 in ground beef within the U.S. population can be developed. The level of detail needed in a risk characterization depends on the type of problem under consideration.

SENSITIVITY ANALYSIS

Sensitivity analysis refers to the quantitative process of identifying factors (model inputs) that are most responsible for influencing the occurrence and extent of *E. coli* O157:H7 in ground beef (model outputs). A combination of statistical, algebraic, and graphical techniques is used to illustrate the effect of sensitive factors on model outputs. Two types of sensitivity analyses are used in this risk assessment: correlation analysis and dependency analysis.

Correlation Analysis

Correlation analysis is used to identify "uncertain" factors (i.e., model inputs for which there are limited data and information) that influence intermediate and final model outputs. Factors that are supported by data and information (i.e., not "uncertain") are identified by dependency analysis (discussed in the next section). Therefore, correlation analysis is but one technique for identifying factors most important in influencing the likelihood of exposure or risk of illness.

Correlation analysis was used to identify "uncertain" factors most important in influencing the occurrence and extent of *E. coli* O157:H7 contamination in ground beef at various points along the farm-to-table continuum:

- *E. coli* O157:H7 in combo bins created from steer/heifer carcasses,
- *E. coli* O157:H7 in combo bins created from cow/bull carcasses,
- *E. coli* O157:H7 in grinder loads,
- *E. coli* O157:H7 in ground beef servings prior to storage and cooking, and
- *E. coli* O157:H7 in ground beef servings after storage and cooking.

For each of these outputs, correlation was measured relative to the number of *E. coli* O157:H7 organisms within a unit (i.e., combo bin, grinder load, or single serving) and the prevalence (%) of *E. coli* O157:H7-contaminated units (i.e., combo bins, grinder loads, servings). The mean number of *E. coli* O157:H7 organisms in a unit (e.g., combo bin) was estimated for each output. Factors were identified as correlated to the output if the Spearman rank correlation coefficient was greater than 0.30.

E. coli O157:H7 in Combo Bins Created from Steer/Heifer Carcasses

The size of the *E. coli* O157:H7-contaminated carcass surface area was the only factor correlated (coefficient = 0.33) with the number of *E. coli* O157:H7 organisms in steer/heifer combo bins (Table 5-3). This correlation only applied to the high prevalence season (June to September). There was no correlation between the extent of carcass contamination and the resulting number of *E. coli* O157:H7-contaminated steer/heifer combo bins. Uncertainty regarding the size of *E. coli* O157:H7 contamination area on carcasses ranged from 40 cm^2 (5th percentile) to 900 cm^2 (95th percentile).

TABLE 5-3 Correlations with *E. coli* O157:H7 Contamination in Steer/Heifer Combo Bins

E. coli O157:H7 Contamination in Steer/Heifer Combo Bins	Output Correlations with the Number of *E. coli* O157:H7 Organisms in a Unit and the Percent of Units Contaminated (%) by Season			
	June to September (High Prevalence Season)		October to May (Low Prevalence Season)	
Model Input (factor)	No.	%	No.	%
Area of carcass contaminated	0.33			

E. coli O157:H7 in Combo Bins Created from Cow/Bull Carcasses

Factors that most influence the occurrence and extent of *E. coli* O157:H7 contamination in cow/bull combo bins are the size of the *E. coli* O157:H7-contaminated carcass surface area and the average (mean) effect of chilling on contaminated carcasses (Table 5-4). The change in the number of *E. coli* O157:H7 organisms resulting from chilling was modeled as a normal distribution with an uncertain mean ranging from –0.5 to +0.5. The effect of chilling the carcasses was correlated with the number of *E. coli* O157:H7-contaminated cow/bull combo bins but not with the number of *E. coli* O157:H7 in these combo bins.

E. coli O157:H7 in Grinder Loads

Factors that most influence the prevalence and number of *E. coli* O157:H7 organisms in grinder loads are (1) the size of the *E. coli* O157:H7-contaminated surface area, (2) the effect of chilling on carcasses, and (3) the prevalence and number of *E. coli* O157:H7 organisms in combo bins (both steer/heifer and cow/bull). Table 5-5 shows that *E. coli* O157:H7 contamination in grinder loads is more correlated with the prevalence and number of *E. coli* O157:H7 organisms in steer/heifer combo bins than cow/bull combo bins. Little to no correlation is found between the average number of *E. coli* O157:H7 organisms in combo bins and the number of *E. coli* O157:H7

TABLE 5-4 Correlations with *E. coli* O157:H7 Contamination in Cow/Bull Combo Bins

E. coli O157:H7 Contamination in Cow/Bull Combo Bins	Output Correlations with the Number of *E. coli* O157:H7 Organisms in a Unit and the Percent of Units Contaminated (%) by Season			
	June to September (High Prevalence Season)		October to May (Low Prevalence Season)	
Model Input (factor)	No.	%	No.	%
Area of carcass contaminated	0.33	0.32		0.34
Mean of chilling distribution		0.37		0.36

TABLE 5-5 Correlations with *E. coli* O157:H7 Contamination in Grinder Loads

E. coli O157:H7 Contamination in Grinder Loads	Output Correlations with the Number of *E. coli* O157:H7 Organisms in a Unit and the Percent of Units Contaminated (%) by Season			
	June to September (High Prevalence Season)		October to May (Low Prevalence Season)	
Model Input (factor)	No.	%	No.	%
Cow/bull combos—expected value		0.69		
Cow/bull combos—% contaminated		0.70		0.36
Area of carcass contaminated		0.32		
Mean of chilling distribution		0.34		
Steer/heifer combos—expected value	0.44	0.81	0.33	0.87
Steer/heifer combos—% contaminated		0.97		0.99

organisms in grinder loads. This may be due to the fact that any given grinder load may contain *E. coli* O157:H7 organisms from multiple combo bins, yet the high numbers of *E. coli* O157:H7 organisms in grinder loads are likely caused by the introduction of high numbers of *E. coli* O157:H7 from just one contaminated combo bin. Therefore, the mixing of combo bins to form grinder loads may decrease the influence of combo bin *E. coli* O157:H7 contamination on the average number of *E. coli* O157:H7 organisms in grinder loads.

E. coli O157:H7 in Ground Beef Servings Prior to Storage and Cooking

The number of *E. coli* O157:H7 organisms in grinder loads is an important factor that greatly influences the prevalence and number of *E. coli* O157:H7 organisms in uncooked ground beef servings before storage (Table 5-6). Such a finding is not surprising because the probability of selecting a ground beef serving with 1 or more *E. coli* O157:H7 organisms is dependent on the number of *E. coli* O157:H7 organisms within the grinder load. Table 5-6 indicates that the number of *E. coli* O157:H7-contaminated grinder loads has some influence on the prevalence and density of *E. coli* O157:H7 in uncooked ground beef servings (coefficient: 0.31 to 0.39, October to May). Grinder loads are considered contaminated if they contain at least 1 *E. coli*

TABLE 5-6 Correlations with *E. coli* O157:H7 Contamination in Ground Beef Servings Before the Effects of Growth and Cooking Are Considered

E. coli O157:H7 in Ground Beef Servings Before Storage and Cooking	Output Correlations with the Number of *E. coli* O157:H7 Organisms in a Unit and the Percent of Units Contaminated (%) by Season			
	June to September (High Prevalence Season)		October to May (Low Prevalence Season)	
Model Input (factor)	No.	%	No.	%
Grinders—expected value	0.99	0.95	0.99	0.95
Steer/heifer combos—expected value	0.44	0.40		0.39
Grinders—% contaminated				0.33
Steer/heifer combos—% contaminated				0.31

O157:H7 organism. Because grinder loads are likely to contain 10,000 pounds or more of ground beef, the presence of 1 *E. coli* O157:H7 organism has little effect on whether an individual ground beef serving becomes contaminated with *E. coli* O157:H7.

In general, the more removed an intermediate output (or input) is from a model output, the less influence it has. For example, the occurrence of *E. coli* O157:H7 in steer/heifer combo bins influences the occurrence in grinder loads (Table 5-5). Also, the occurrence of *E. coli* O157:H7 in grinder loads influences the occurrence in servings prior to growth and cooking (Table 5-6). Therefore, the greater influence of *E. coli* O157:H7-contaminated grinder loads relative to *E. coli* O157:H7-contaminated combo bins on the occurrence and extent of *E. coli* O157:H7 contamination in ground beef servings (Table 5-6) simply reflects the closer proximity of ground beef in grinders to ground beef servings in the farm-to-table continuum.

E. coli O157:H7 in Ground Beef Servings After Storage and Cooking

Factors that most influence the occurrence and extent of *E. coli* O157:H7 contamination in consumed ground beef servings (dose) are the prevalence and number of *E. coli* O157:H7 organisms in ground beef servings before storage, the type of storage (e.g., refrigeration versus freezing), the average amount of growth (or decline) in *E. coli* O157:H7 during storage of ground beef servings, and the effect of cooking.

Cooking is notable in its absence from Table 5-7. The effectiveness of cooking is poorly correlated with the exposure distribution in this type of sensitivity analysis because it does not have a wide range of uncertainty (e.g., uncertainty of less than 1 log). In contrast, there is greater uncertainty regarding the growth of *E. coli* O157:H7 during storage (e.g., uncertainty of as much as 2 logs). As a result, the effect of cooking on the amount of *E. coli* O157:H7 in contaminated ground beef servings is revisited in another type of sensitivity analysis (dependency analysis) in the next section.

The uncertainty related to the maximum population density of *E. coli* O157:H7 in ground beef strongly influences the density of *E. coli* O157:H7 in consumed servings (Table 5-7). Uncertainty about the maximum population density for *E. coli* O157:H7 in ground beef servings can range from 5 to 10 logs. This large uncertainty, combined with the importance of this input in the model, accounts for the magnitude of the correlation coefficient (coefficient: 0.58 to 0.60).

TABLE 5-7 Correlations with *E. coli* O157:H7 Contamination in Ground Beef Servings After the Effects of Growth and Cooking Are Considered

E. coli O157:H7 in Ground Beef Servings After Storage and Cooking	Output Correlations with *E. coli* O157:H7 Density and Percent of Units Contaminated (%) by Season			
	June to September (High Prevalence Season)		October to May (Low Prevalence Season)	
Model Input (factor)	Density	%	Density	%
Grinders—expected value	0.35	0.79	0.44	0.78
Max pop density	0.58		0.60	
Growth—expected value	0.82		0.85	
Home/HRI storage temperatures	(0.31)			
Servings before growth and cooking—expected value	0.36	0.78	0.45	0.76
Servings before growth and cooking—% contaminated		0.77	0.39	0.78
Percent ground beef frozen		(0.40)		(0.43)
Steer/heifer combos—expected value		0.36		

The percent of ground beef that is frozen is negatively correlated with the prevalence or density of *E. coli* O157:H7 in consumed servings (Table 5-7). Freezing directly reduces *E. coli* O157:H7 in servings (Sage and Ingham 1998). However, freezing also makes *E. coli* O157:H7 somewhat more heat stable, thereby reducing cooking effectiveness.

The number of *E. coli* O157:H7 organisms in consumed ground beef servings is negatively correlated with home/HRI storage temperatures (Table 5-7). This distribution is modeled using cumulative probabilities. A negative correlation results because lower cumulative probability values are associated with increased occurrence of higher storage temperatures and, consequently, more growth of *E. coli* O157:H7 in ground beef servings.

Previous intermediate outputs, such as grinders, servings before growth and cooking, and steer heifer combos, also influence the occurrence of *E. coli* O157:H7 in consumed ground beef servings (Table 5-7).

Although correlation is one measure of sensitivity, it does not address important inputs that are fixed or relatively certain. The correlation analysis completed for this risk assessment suggests that the *E. coli* O157:H7-contaminated carcass surface area (during slaughter), the average effectiveness of chilling carcasses (slaughter), the maximum population density for *E. coli* O157:H7 in ground beef servings, and home storage (e.g., refrigeration) temperatures are important factors that may influence the occurrence of *E. coli* O157:H7 in consumed ground beef servings and subsequent risk of illness. Nevertheless, some inputs are less uncertain (e.g., cooking effectiveness), yet might be very influential on the exposure to *E. coli* O157:H7 in ground beef and the subsequent risk of illness. Therefore, another type of sensitivity analysis is conducted to identify other factors important in influencing the occurrence of *E. coli* O157:H7 in ground beef and the subsequent risk of illness. This alternative is termed dependency analysis.

Dependency Analysis

Dependency analysis provides insight into the importance of various factors along the farm-to-table continuum that ultimately influence the risk of illness from *E. coli* O157:H7 in ground beef. This type of sensitivity analysis considers the effect of changing parameters for specific factors (model inputs) and examines their effect on intermediate model outputs (occurrence and extent of *E. coli* O157:H7 contamination).

Although some factors (model inputs) do not appear to be correlated (*correlation analysis*) with the occurrence of *E. coli* O157:H7 in consumed ground beef servings and subsequent risk of illness (model outputs), the model outputs might still largely depend (*dependency analysis*) on the values of these inputs. As an example, decontamination steps in slaughter influence the number of *E. coli* O157:H7 organisms remaining on a carcass just prior to trim being generated and placed in combo bins. This effect of decontamination is algebraically determined in the model. However, the parameters describing how decontamination effectiveness varies between carcasses are not very uncertain (varying by only a 0.5 log reduction). In contrast, the most likely value for maximum *E. coli* O157:H7 population density can vary over a 5.0 log range. Therefore, uncertainty about decontamination effectiveness is not substantial enough (i.e., correlation >0.30) to be identified, through correlation analysis, as an important factor influencing the prevalence and number of *E. coli* O157:H7 in combo bins. Instead, this factor would be identified through the use of dependency analysis.

Because this risk assessment involves complicated relationships among model inputs, dependency analysis illustrates the effect of changing model inputs on intermediate model outputs (i.e., the occurrence and extent of *E. coli* O157:H7 contamination in ground beef along the farm-to-table continuum). The analysis is conducted by developing different scenarios where some model inputs are intentionally changed and the resultant outputs are compared with model outputs generated from a baseline scenario (i.e., where all model inputs are unchanged).

Production and Slaughter Modules

Because production and slaughter module inputs both influence the *E. coli* O157:H7 contamination that occurs in combo bins, their dependency analysis is completed in tandem.

This analysis is limited to simulating steer/heifer slaughter establishments during the high prevalence season (June to September). The simulations only consider cattle contaminated during the dehiding step in slaughter. Model inputs that are not evaluated in the dependency analysis are held at their median values.

Although the scope of this dependency analysis is limited, it is reasonable to assume that its results will also describe proportional changes occurring in cow/bull slaughter plants, as well as in both types of plants during the low prevalence season. Besides feedlot and within-feedlot prevalence, no other model inputs to the slaughter module differ dramatically between the seasons.

Simulated Scenarios for Production and Slaughter

Scenarios were simulated that change, in turn, feedlot *E. coli* O157:H7 prevalence, within-feedlot *E. coli* O157:H7 prevalence, decontamination following dehiding, steam pasteurization following evisceration, the live cattle to carcass transformation ratio, and the effect of carcass chilling. Changes to these model inputs for each scenario were as follows:

- *Feedlot prevalence scenario*—changes the value for feedlot *E. coli* O157:H7 prevalence from 88% to 44% (a 50% change).

- *Within-feedlot scenario*—changes the value for average within-feedlot *E. coli* O157:H7 prevalence from 22% to 11% (50% change).
- *Decontamination following dehiding scenario*—changes the effectiveness of decontamination from a most likely range of 0.3 and 0.7 logs (baseline) to a uniform decontamination effectiveness of 1.2 logs (i.e., assumes there is always maximum effectiveness of decontamination following dehiding).
- *Steam pasteurization scenario*—changes the effectiveness of decontamination from a most likely range of 0.5 to 1.5 logs (baseline) to a uniform decontamination effectiveness of 2.5 logs (i.e., assumes there is always maximum effectiveness of steam pasteurization).
- *Live cattle to carcass transformation ratio scenario*—changes the distribution ranging from 1 to 2 to a constant of 1 (i.e., this scenario assumes a lowest possible ratio of *E. coli* O157:H7-contaminated carcasses to infected live cattle). This scenario suggests greater control of *E. coli* O157:H7 contamination during the dehiding step when live cattle are converted to carcasses.
- *Carcass chilling effect scenario*—changes the standard deviation for chilling in the baseline scenario to zero (i.e., assumes carcass chilling has no effect in either increasing or decreasing the number of *E. coli* O157:H7 organisms on carcasses). Although correlation analysis has already shown that the carcass chilling step is important in predicting *E. coli* O157:H7 contamination in combo bins, a scenario for this input is simulated for illustration.

Results of the Simulated Scenarios for Production and Slaughter

Figure 5-4 shows the results of these scenario analyses. All of the scenarios resulted in a lower number of *E. coli* O157:H7-contaminated combo bins compared with the baseline scenario (i.e., no changes). That is, all scenarios resulted in less than 40% (baseline) of combo bins containing 1 or more *E. coli* O157:H7 organisms.

The most effective decontamination scenario was the assumption of a 2.5 log reduction in the number of *E. coli* O157:H7 organisms on carcasses from steam pasteurization. The *steam pasteurization scenario* resulted in a 75% reduction in the number of *E. coli* O157:H7-contaminated combo bins compared with the baseline scenario. The *decontamination following dehiding scenario* results in about an 50% reduction in the number of *E. coli* O157:H7-contaminated combo bins compared with the baseline scenario. Both decontamination after dehiding and steam pasteurization generally reduced the number of *E. coli* O157:H7 organisms on contaminated carcasses and in subsequent combo bins. Steam pasteurization has a greater influence than decontamination after dehiding in these scenarios because its effectiveness is 2.5 logs versus 1.2 logs for decontamination after dehiding.

Reducing feedlot prevalence by 50% results in a 43% reduction in the number of *E. coli* O157:H7-contaminated combo bins. A similar reduction in within-feedlot prevalence results in only a 25% reduction in the number of *E. coli* O157:H7-contaminated combo bins. Feedlot prevalence determines the proportion of truckloads that arrive with one or more infected cattle. Within-feedlot prevalence is variable between contaminated truckloads, and it determines how many infected cattle there are among the 40-head capacity of these trucks. Therefore, the influence of feedlot prevalence on the incoming prevalence of infected cattle is somewhat more direct than the influence of within-feedlot prevalence.

The distribution for the *transformation ratio scenario* generally parallels the distribution for the within-feedlot prevalence scenario but is slightly less effective. On average, there are about 1.5 *E. coli* O157:H7-contaminated carcasses per infected live animal (e.g., cross-contamination).

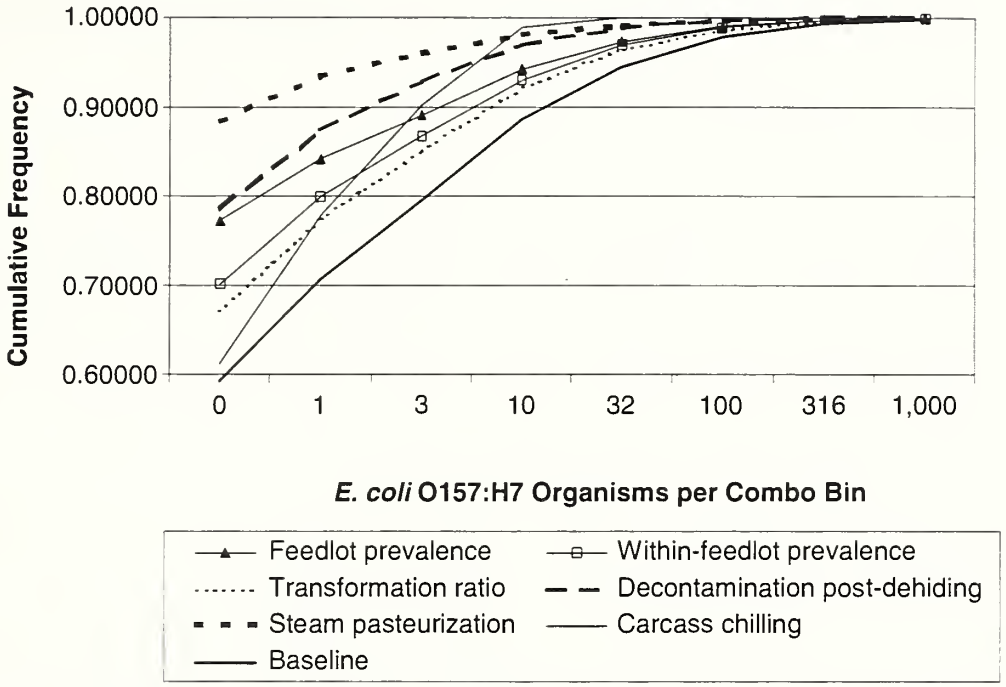

FIGURE 5-4 Comparison of cumulative distributions of combo bin contamination for six scenarios relative to baseline. Feedlot and within-feedlot prevalence scenarios reduce these inputs by 50%. The decontamination and steam pasteurization scenarios assume a constant maximum effectiveness of these steps.

Therefore, this scenario assumes about a one-third reduction in this input relative to the baseline scenario. This magnitude of reduction is less than that resulting from the 50% reduction in within-feedlot prevalence and explains the discrepancy between the respective distributions. It is expected that modeling a 50% reduction in the transformation ratio would result in a shift in the combo bin contamination distribution similar to that shown for the within-feedlot prevalence scenario. However, a 50% reduction in the transformation ratio would be beyond the bounds of the current uncertainty distribution.

Carcass chilling had little effect on the number of *E. coli* O157:H7-contaminated combo bins. However, in this scenario, there was a dramatic reduction in the occurrence of high levels of *E. coli* O157:H7 in combo bins relative to other scenarios. Because the influence of carcass chilling on individual combo bins can range from –3 to +3 logs in the baseline scenario, this step can result in substantial amplification of *E. coli* O157:H7 on carcasses and in combo bins. This scenario illustrates that high numbers of *E. coli* O157:H7 organisms in combo bins are primarily the result of increases in the number *E. coli* O157:H7 organisms on carcasses during chilling. Furthermore, this scenario illustrates that the high numbers of *E. coli* O157:H7 organisms in combo bins are influenced by the high numbers of *E. coli* O157:H7 organisms that occur occasionally on chilled carcasses. This suggests that chilling carcasses is an important factor that greatly influences the number of *E. coli* O157:H7 in beef trim in combo bins.

While all of these factors are important in influencing *E. coli* O157:H7 contamination in ground beef, it may be more important to focus mitigation strategies on areas that influence the occurrence of *E. coli* O157:H7-contaminated ground beef servings (e.g., steam pasteurization) than on those that influence the number of *E. coli* O157:H7 in a contaminated serving (e.g., carcass chilling). As noted in the "*Risk of E. coli O157:H7 Illness as a Function of Exposure*

(Dose)" section, population risk of illness may be influenced more by prevalence of *E. coli* O157:H7-contaminated ground beef servings than by the level of *E. coli* O157:H7 in contaminated servings (dose).

Preparation Module

The preparation module primarily consists of creating, storing, and cooking ground beef servings. In the correlation analysis, storage temperature, proportion of ground beef that is frozen, and the amount of growth during storage were the most influential factors contributing to the occurrence and extent of *E. coli* O157:H7 in consumed ground beef servings (Table 5-7). However, there was no demonstrated correlation with cooking temperature or the log reduction expected from cooking. Therefore, the effects of cooking temperature and storage conditions on the occurrence and extent of *E. coli* O157:H7 contamination in consumed ground beef servings is considered as part of "what if" scenarios (dependency analysis).

Simulated Scenarios for Preparation

The following scenarios were considered:

1. *No growth during storage scenario*—assumes that all ground beef servings are stored to ensure that no growth takes place at retail, from retail to the home/HRI, and while stored at the home/HRI.
2. *Cooking to 5 log reduction scenario*—assumes that all ground beef servings are cooked to ensure at least a 5 log reduction in *E. coli* O157:H7 organisms. In this scenario, the median cooking distribution is applied except for those ground beef servings that would have less than a 5 log reduction. These ground beef servings are modeled such that a 5 log reduction occurs.
3. *No growth during storage and 5 log reduction during cooking scenario*—assumes all ground beef servings are stored to ensure that no growth takes place and, in addition, are all cooked to ensure at least a 5 log reduction in *E. coli* O157:H7 organisms.

Results of the Simulated Scenarios for Preparation

Figure 5-5 shows the median exposure distribution from the baseline model and the resultant exposure distributions from each of the three scenarios in this sensitivity analysis. Each scenario results in a reduction in the prevalence of *E. coli* O157:H7-contaminated servings relative to the baseline scenario. The *no growth during storage scenario* results in a 7% decrease in the number of *E. coli* O157:H7-contaminated ground beef servings. The *cooking to 5 log reduction scenario* results in a 93% decrease in the number of *E. coli* O157:H7-contaminated servings. The third scenario, combining the effect of no growth during storage and cooking to a 5 log reduction, results in a 99.99% decrease in the number of *E. coli* O157:H7-contaminated ground beef servings.

Ensuring at least a 5 log reduction from cooking reduces the maximum number of *E. coli* O157:H7 organisms per ground beef serving (dose) to which individuals could be exposed. Exposures that remain after all servings have at least a 5 log reduction applied demonstrate that there can be enough growth to overcome the effect of cooking. Ensuring that no growth takes place also reduces the maximum dose of *E. coli* O157:H7 in ground beef to which individuals could be exposed. In this case, there can be no more *E. coli* O157:H7 organisms in a ground beef serving than were originally present when the servings were generated from grinder loads. Because a small proportion (4% to 8%) of the U.S. population grossly undercooks (i.e., little or

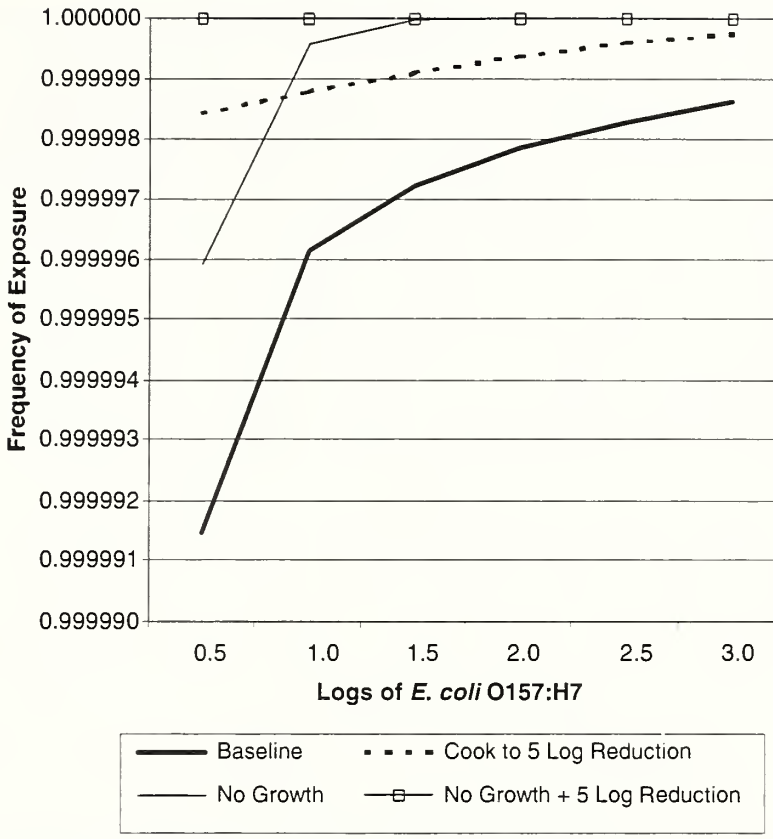

FIGURE 5-5 Reduction in the number of *E. coli* O157:H7 organisms per ground beef serving for three scenarios relative to a baseline scenario. One scenario assumes no growth of *E. coli* O157:H7 during storage. The second scenario assumes that cooking of all products ensures at least a 5 log reduction. The third scenario combines no growth and a 5 log reduction from cooking.

no log reduction in the number of *E. coli* O157:H7) ground beef servings, the *no growth during storage scenario* still allows exposure of up to 2 logs of *E. coli* O157:H7 per ground beef serving.

Virtually no risk of *E. coli* O157:H7 illness exists if ground beef servings are handled in such a way that no growth occurs and are cooked in such a way as to ensure a minimum of a 5 log reduction in the number of *E. coli* O157:H7 organisms. Such a finding may be reassuring to consumers. However, since consumers do not have complete control over the product (i.e., storage conditions at retail), it is possible for sufficient growth to take place that a 5 log reduction through cooking is not enough to render the product safe.[13]

Comparing the effects of storage and cooking implied by this analysis suggests that ensuring adequate cooking may be more important than controlling the growth of *E. coli* O157:H7 in servings. Cooking was not identified in the correlation analysis. Demonstrating its importance, therefore, requires dependency analysis. Furthermore, this dependency analysis has clearly shown that controlling both cooking and growth can substantially reduce the probability of exposure to *E. coli* O157:H7 in ground beef.

[13]FSIS recommends that consumers cook their hamburgers to 160°F (internal product temperature) and use a meat thermometer.

CONCLUSIONS

The *E. coli* O157:H7 risk assessment is a practical tool that can be used to evaluate various intervention strategies to control and prevent the occurrence and extent of *E. coli* O157:H7 contamination in ground beef. This risk characterization provides information on the risk of illness from *E. coli* O157:H7 in ground beef for an individual, a community, and the entire U.S. population. Variability in the population risk of illness from *E. coli* O157:H7 in ground beef is considered based on differences in seasonal exposure and age of the consumer. The risk characterization also provides information regarding which factors have the greatest influence on the occurrence of *E. coli* O157:H7 in combo bins, grinder loads, and ground beef servings and on subsequent risk of illness. The results of the risk characterization are summarized below.

Risk of Illness from *E. coli* O157:H7 in Ground Beef

- An illustrative example of the risk of illness from *E. coli* O157:H7 in ground beef was used to show how this model could calculate risk for individuals. A "typical" individual's annual risk of illness from *E. coli* O157:H7 in ground beef is between 1 in 600 million servings and 1 in 400 billion servings.
- The *E. coli* O157:H7 risk assessment was used to illustrate a foodborne outbreak scenario for a community in which a grinder load of ground beef was stored improperly and the number of *E. coli* O157:H7 in it reached 5.5 logs per serving. If all of these servings were undercooked (e.g., served by the same restaurant) and individuals consume only one of these servings, then about 3,200 people would be expected to become ill. On the other hand, if all of these contaminated ground beef servings had been subjected to similar cooking conditions that resulted in a decrease of 5.5 logs, only 12 people would be expected to become ill from *E. coli* O157:H7.
- The annual risk of illness from *E. coli* O157:H7 in ground beef for the general U.S. population is nearly 1 illness in 1 million servings of ground beef (9.6×10^{-7}). This corresponds to a risk of being hospitalized and recovering of 2.0×10^{-8} per serving, developing HUS and recovering of 4.2×10^{-9} per serving, and death of 5.9×10^{-10} per serving.
- Most contaminated cooked ground beef servings contain only 1 *E. coli* O157:H7 organism. The subsequent probability of illness given an exposure of 1 *E. coli* O157:H7 organism in a ground beef serving is low. Therefore, this results in a low risk of illness from *E. coli* O157:H7 in a ground beef serving.
- Few contaminated cooked ground beef servings contain 100,000 *E. coli* O157:H7 organisms per serving (1.8×10^{-7}). The probability of illness at this dose is 0.58. This results in the highest risk of illness (1.0×10^{-7}) from *E. coli* O157:H7 in a ground beef serving (see Table 5-1 and Figure 5-1).
- Reducing the number of *E. coli* O157:H7-contaminated ground beef servings may reduce risk of illness more than reducing the amount of *E. coli* O157:H7 in contaminated servings.

Population Risk Variabilty

- The risk of *E. coli* O157:H7 illness is about three times higher during June to September than during October to May.

- The risk of *E. coli* O157:H7 illness is, hypothetically, about 2.5 times higher for children ages 0 to 5 (2.4×10^{-6} per serving) than for the general U.S. population (9.6×10^{-7}). This estimate is based on the assumption that children under 5 years of age are more susceptible to illness from exposure to *E. coli* O157:H7 while consuming only about 7% of all ground beef servings and smaller serving sizes.

Sensitivity Analysis

Correlation Analysis

- The size of the *E. coli* O157:H7-contaminated carcass surface area is an important factor that most influences the occurrence of *E. coli* O157:H7 in steer/heifer combo bins (see *Sensitivity Analysis*, Table 5-2).
- The size of the *E. coli* O157:H7-contaminated carcass surface area and the effects of carcass chilling are factors that most influence the occurrence of *E. coli* O157:H7 in cow/bull combo bins (see *Sensitivity Analysis*, Table 5-3).
- The occurrence and extent of *E. coli* O157:H7 contamination in cow/bull and steer/heifer combo bins, the size of the *E. coli* O157:H7-contaminated carcass surface area, and the effects of carcass chilling are factors that most influence the occurrence of *E. coli* O157:H7 in grinder loads (see *Sensitivity Analysis*, Table 5-4).
- The occurrence of *E. coli* O157:H7 in grinder loads and in steer/heifer combo bins are factors that most influence the occurrence of *E. coli* O157:H7 in uncooked ground beef servings (see *Sensitivity Analysis*, Table 5-5).
- The number of *E. coli* O157:H7 organisms in steer/heifer combo bins and grinder loads as well as the maximum population density for *E. coli* O157:H7 per ground beef serving, growth of *E. coli* O157:H7 during storage and handling, storage temperatures, and the percent of ground beef that was frozen are factors that most influence the occurrence and extent of *E. coli* O157:H7 in consumed ground beef servings (see *Sensitivity Analysis*, Table 5-6).

Dependency Analysis

- If steam pasteurization was 100% effective (e.g., always resulted in a 2.5 log reduction in the number of *E. coli* O157:H7 organisms on carcasses), then the number of *E. coli* O157:H7-contaminated combo bins would decline by 75% compared with the baseline scenario. This was the most effective scenario considered in reducing the number of *E. coli* O157:H7-contaminated combo bins.
- If decontamination following dehiding always maintained a maximum effectiveness of a 1.2 log reduction in the number of *E. coli* O157:H7 organisms on carcasses, then the number of *E. coli* O157:H7-contaminated combo bins would decrease 50% (see *Sensitivity Analysis*, Figure 5-4).
- Reducing feedlot prevalence by 50% results in a 43% reduction in the number of *E. coli* O157:H7-contaminated combo bins. A similar reduction in within-feedlot prevalence results in only a 25% reduction in the number of *E. coli* O157:H7-contaminated combo bins (see *Sensitivity Analysis*, Figure 5-5).
- Carcass chilling had little effect on the number of *E. coli* O157:H7-contaminated combo bins but had a large effect on the amount of *E. coli* O157:H7 in contaminated combo

bins. Large numbers of *E. coli* O157:H7 organisms in combo bins are primarily the result of occasionally high numbers of *E. coli* O157:H7 on chilled carcasses (e.g., improper chilling) (see *Sensitivity Analysis*, Figure 5-6).

- Both growth of *E. coli* O157:H7 in contaminated ground beef servings during storage and reduction in the number of *E. coli* O157:H7 organisms during cooking are factors that most influence the occurrence and extent of *E. coli* O157:H7 contamination in ground beef servings. The dependency analysis indicates that adequate cooking may be more important than controlling the growth of *E. coli* O157:H7 in ground beef servings. Virtually no risk of *E. coli* O157:H7 illness exists from ground beef servings that are stored and handled under conditions that do not allow growth to occur and are sufficiently cooked to ensure a minimum of a 5 log reduction in the number of *E. coli* O157:H7 organisms (see *Sensitivity Analysis*, Figure 5-5).

LIMITATIONS

When approaching this risk assessment, it is important to understand its scope, purpose, and data limitations. First, the scope of this risk assessment was limited to ground beef because epidemiological evidence indicated it was the primary foodborne vehicle for exposure to *E. coli* O157:H7 (see Chapter 2). Ground beef servings were those from patties, sandwiches, meat loaf, and meatballs in which the ground beef could potentially be undercooked and have viable *E. coli* O157:H7. Foods consisting of granulated ground beef and intact and nonintact (e.g., tenderized) cuts of beef, such as steaks and roasts, were not included in the risk assessment. These foods were excluded because the associated risk of exposure to *E. coli* O157:H7 is thought to be low based on epidemiological evidence and input from the National Advisory Committee for Microbiological Criteria for Foods (NACMF, December 2000). This risk assessment, however, will be used to develop risk assessments for *E. coli* O157:H7 in other beef products (e.g., nonintact beef).

Second, the effect of differences in the food matrix on *E. coli* O157:H7 survival and growth were not included in this risk assessment because of lack of data. Although the included ground beef products are similar, matrix differences such as salt, water activity, pH, and spices likely vary between these foods.

Third, the contribution of cross-contamination to *E. coli* O157:H7 exposure was also not included due to a lack of data. For example, there is little to no information about the proportion of foodborne outbreaks or sporadic cases of *E.* coli O157:H7 infection that are due to exposure to a nonbeef food item that was cross-contaminated by beef (e.g., lettuce). Cross-contamination of salad bar and other food items was thought to be the cause of four outbreaks that occurred in four separate restaurants in two states during 1993–1994 (Jackson et al. 2000). Interestingly, the implicated beef item in these outbreaks was not ground beef but was an intact cut of beef that was tenderized by maceration at the restaurant.

Fourth, the derivation of the dose-response function in hazard characterization was based on *E. coli* O157:H7 illnesses in the general population without further differentiation for sensitive subpopulations, such as children or the elderly. While it was assumed that children ages 0 to 5 are more susceptible and might have a dose-response function similar to the *E. coli* O157:H7 dose-response upper bound function (derived from *Shigella dysenteriae* clinical studies), supporting foodborne illness surveillance data are needed to validate this assumption.

Finally, the derived *E. coli* O157:H7 dose-response function did not take into consideration any differences in pathogenicity among *E. coli* O157:H7 strains.

RESEARCH NEEDS

An important benefit of conducting a risk assessment is the identification of data and knowledge gaps. Through the collection and evaluation of data for this risk assessment, it became apparent that specific information and data would enhance the certainty of the risk assessment estimates. The determination of which data would be most beneficial is based on areas identified as important (sensitivity analysis) *and* for which there is limited information. Food safety research needed to fill existing data gaps and enhance this risk assessment is discussed below.

Hazard Identification

- Information on the maximum density of *E. coli* O157:H7 organisms in ground beef servings as a result of matrix effects, competitive microflora in ground beef, and environmental conditions (e.g., pH, water activity).[14]
- Predictive microbiological data on the increase and decrease in the number of *E. coli* O157:H7 organisms in ground beef under various storage and preparation conditions along with frequencies of occurrence of these storage and preparation conditions.

Exposure Assessment

- Additional information on *E. coli* O157:H7 contamination on carcasses following dehiding.
- Data on cross-contamination of *E. coli* O157:H7 between carcasses during carcass splitting.
- Time-temperature data (quantitative) for chillers in slaughter establishments.
- Marketing data on the proportion of beef ground at slaughter versus at retail.
- Data on retail (HRI) and consumer storage, cooking, and consumption (frequency and serving size) patterns by type of ground beef meal (e.g., grilled hamburger in July and baked meat loaf in October).

Hazard Characterization (Dose-Response Data)

- Number and severity of illness among children ages 0 to 5 from *E. coli* O157:H7 in ground beef (response data). These data may come from surveillance data or from foodborne outbreak data.[15]
- Dose-response data from foodborne outbreaks of *E. coli* O157:H7 in ground beef servings (e.g., the number of *E. coli* O157:H7 organisms in a serving and resulting severity of illness).

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[14]There is considerable uncertainty regarding the maximum population density in ground beef servings due to competitive microflora (see Chapter 3). The risk assessment includes an uncertainty range of 5 to 10 logs of *E. coli* O157:H7 for the maximum population density in ground beef servings.

[15]For all outbreaks, the line listing should include month and year of occurrence and the number of ill persons per outbreak. For foodborne outbreaks, the line listing should include month and year of outbreak occurrence, county and state of occurrence, number of ill persons, number hospitalized, number with severe outcome (e.g., stillbirth/miscarriage for *Listeria monocytogenes*, HUS/TTP for *E. coli* O157:H7), number of deaths, specific vehicle implicated (e.g., not just "beef" but ground beef, roast beef etc.), and detailed comments about sensitive subpopulations, (e.g., immunocompromised persons in an outbreak of *L. monocytogenes*, ages of persons with HUS, age and health status of persons who died).

- Descriptive epidemiologic information about sporadic cases of *E. coli* O157:H7 illness, including the month of disease onset, age, sex, hospitalizations, summary of clinical manifestations including severe disease manifestations, and food vehicles involved (if known).
- Additional case-control studies of sporadic *E. coli* O157:H7 cases to calculate etiologic fraction attributable to ground beef.

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Appendix A

Anchoring of Model Parameters

INTRODUCTION

The *Escherichia coli* O157:H7 risk assessment model is essentially a process risk model that describes the occurrence and levels of this pathogen across the farm-to-table continuum. All such models include parameters that are intended to be deterministic. However, knowledge about these parameters is often uncertain.

The resolution for each model parameter depends on the quantity and quality of the data available about that parameter. Different data types and sources are often used to estimate the various parameters in the model. As described in this report, each *E. coli* O157:H7 risk assessment model parameter was independently calibrated from available evidence and scientific knowledge. During the model development stage, however, parameter calibration did not include consideration of the model outputs.

Because the parameters are independently calibrated from data of varying quality and quantity, it is expected that there are combinations of these parameters that, when used in the model, predict outcomes that are entirely inconsistent with what has been observed. The knowledge used to describe the uncertainty about parameters before running the model is less than that available after running the model. After running the model, it becomes clear that some parameter values are not feasible given the available evidence about the model's output. These infeasible values, or combinations of values, should be used to improve the resolution of the input parameters and, consequently, the model's predictions. The evidence used to define infeasible values is often referred to as validation data.

One output of the *E. coli* O157:H7 risk assessment model for which validation data exist is the prevalence of *E. coli* O157:H7-contaminated grinder loads. Since 1994, the Food Safety and Inspection Service (FSIS) has treated various raw chopped or ground beef products that contain *E. coli* O157:H7 as adulterated under the Federal Meat Inspection Act unless they are further processed in a manner that destroys this pathogen. In October 1994, FSIS initiated a

microbiological testing program for *E. coli* O157:H7 in raw ground beef in meat plants and retail stores. The testing program operated under FSIS Notice 50-94, issued December 23, 1994, until the agency issued FSIS Directive 10,010.1 on February 1, 1998. Based on the low concentrations of *E. coli* O157:H7 recovered from samples of frozen ground beef patties identified in a 1993 outbreak, FSIS increased the sample size from 25 grams to 325 grams in FY 1998 to enhance efficiency and the likelihood of detecting pathogens in raw ground beef sold to consumers. In September 1999, microbiologic testing was changed to include immunomagnetic separation methods.

Approximately 1,900 plants under FSIS inspection produce ground beef. Each month, FSIS randomly selects an appropriate number of inspected plants for sample collection. The sampling plan is based on information from Centers for Disease Control and Prevention (CDC) sentinel sites, historic data on foodborne illness outbreaks, and other information. If a plant initiates its own routine sampling program, has a certification from suppliers that the product was tested, or uses in-plant validated pathogen reduction interventions on beef carcasses, FSIS will not collect samples.

The ground beef sampling data can only calibrate those parts of the model that describe events leading up to the creation of grinder loads. Therefore, most of the parameters described for the preparation module are not informed by these data. Nevertheless, because the inputs to the preparation module are calibrated, its outputs are influenced by these data. The outputs include distributions that describe the frequency of exposure to different doses of *E. coli* O157:H7 in ground beef servings.

METHODS

Uncertainty about each model input is described in the three exposure assessment modules. Various probability density functions are used to capture this input uncertainty. Generically, these distributions are summarized by $p\left(\hat{\theta} \mid y_{\hat{\theta}}\right)$, where $\hat{\theta}$ represents a vector of all i inputs and $y_{\hat{\theta}}$ is the evidence available to estimate each $\hat{\theta}_i$ (Green et al. 2000).

Before the production and slaughter modules are run, uncertainty about the prevalence of contaminated grinder loads is based on 2000 FSIS ground beef sampling data (Table A-1). These data are used because they represent an entire year, incorporate the same sampling and testing methods, and are based on very sensitive culture methods.

Ground beef sampling results depict apparent prevalence. As noted previously, apparent prevalence is less than true prevalence because sample size and culture methods do not ensure that every sample from a contaminated source contains organisms or that the laboratory methods will detect those organisms present in the sample. The FSIS sampling data—when assumed to be beta distributed (Vose 1996)—predict the mean annual apparent prevalence as 0.52% with 5th and 95th percentile values of 0.36% and 0.71%, respectively. The seasonal results demonstrate that there were significantly more positive samples in the high prevalence season (June to September) than in the low prevalence season (October to May).

This output uncertainty can be generically summarized as $p(\phi|y_\phi)$, where ϕ is the prevalence of positive ground beef samples given y_ϕ, the appropriate seasonal sampling evidence.

TABLE A-1 FSIS Ground Beef Sampling Results for 2000. These 325-gram samples were collected in federally inspected ground beef processing plants.

Season	Positive	Tested	5th Percentile	Mean	95th Percentile
Low prevalence (October–May)	10	3,139	0.20%	0.35%	0.54%
High prevalence (June–September)	13	1,447	0.59%	0.97%	1.42%
Annual	23	4,586	0.36%	0.52%	0.71%

A method for calibrating process models using input and output uncertainty has been reported (Green et al. 2000). Before running the model, the joint probability of the inputs and outputs is represented by $p(\phi, \hat{\theta} \mid y_\phi, y_{\hat{\theta}}) = p(\phi \mid y_\phi) \times p(\hat{\theta} \mid y_{\hat{\theta}})$. In other words, the probability of different combinations of input values and output values is predicted independently from each input and output distribution. Before running the model, therefore, the joint probability of a more likely input value and a more likely output value is greater than the joint probability of less likely values from the input or output distribution or both.

When simulated in sequence, the production and slaughter modules generate distributions for levels of *E. coli* O157:H7 in combo bins. The preparation module simulates mixing combo bins to generate grinder loads with varying levels of *E. coli* O157:H7. For calibration, the model output of interest is the prevalence of positive samples from grinder loads.

Sampling from grinder loads is simulated to mimic the FSIS methods by assuming 325-gram samples and the current FSIS culture methods. The probability that a sample contains x organisms is predicted by *Poisson* (325 × GLC), where GLC is the grinder load concentration described in the preparation module. The probability of a positive test equals $1-(1-s)^x$, where s is the probability that laboratory methods detect a single organism in a sample.

Evidence concerning the likelihood of detecting *E. coli* O157:H7 in ground beef comes from an experimental study (Okrend et al. 1990). In that study, 25-gram samples of ground beef were each inoculated with an average of 18 *E. coli* O157:H7, and eight of nine samples (89%) were positive. The probability of a positive sample was assumed to equal $1-(1-s)^{18}$. In this case, s equaled 0.11. The 2000 FSIS sampling results reflect the use of immunomagnetic separation methods in addition to culture. On the basis of discussions with FSIS microbiologists, it is assumed that s is four times greater than methods described in Okrend et al. (1990).

The model selects random combinations of inputs to predict an output. Therefore, the model (M) transforms inputs into outputs (i.e., $M(\hat{\theta}) \rightarrow \phi$). Before running the model, all combinations of inputs and outputs were possible. After running the model, certain combinations are not supported. For example, combinations of inputs that predict high prevalence and high levels of *E. coli* O157:H7 in combo bins cannot result in a model prediction of low apparent prevalence in ground beef. The joint probability of these combinations must be zero. The joint probabilities of combinations that are supported by the model are proportional to their premodel probabilities. Therefore, the most feasible combinations are those that predict apparent prevalence levels consistent with the sampling evidence.

To calibrate the model, the following steps are taken:

1. A random draw from each uncertain parameter is taken.
2. The production, slaughter, and preparation modules are simulated for 10,000 iterations each.

3. For each grinder load concentration (GLC_i) simulated, the probability of a positive test is calculated as $P_{GLC_i}(+) = \sum_{x=0}^{\infty}[1-(1-s)^{x_i}]\times f(x)$, where $s = 0.44$ and

$$f(x) = \frac{(325\times GLC_i)^x \times e^{-325\times GLC_i}}{x!}.$$

4. The prevalence of positive ground beef samples is calculated as $P(+) = \sum_{GLC_{min}}^{GLC_{max}} P_{GLC_i}(+)\times f(GLC_i)$, where $f(GLC_i)$ is the frequency of each GLC (in half-log increments) predicted by the model.
5. If the calculated $P(+)$ for the simulation is less than the 95th percentile of the FSIS ground beef sampling evidence for the appropriate season (Table A-1), then the simulation is considered to represent a feasible combination of inputs. Otherwise, that combination is considered infeasible.
6. If the calculated $P(+)$ for the simulation is less than the 5th percentile of the FSIS ground beef sampling evidence for the appropriate season (Table A-1), then each GLC_i is incrementally increased by 0.5 logs until $P(+)$ is as close to the mean of the ground beef sampling evidence as possible. This adjustment serves to estimate the effect of the fabrication step of the slaughter module.
7. Steps 1 through 6 are repeated until a sufficient set of feasible combinations is collected.

The feasible set of production and slaughter inputs is perpetuated through the preparation module to predict exposure distributions.

RESULTS

Figure A-1 shows the similarity between the distribution for prevalence of positive ground beef samples based on FSIS sampling evidence for the low prevalence season and that estimated after running the model. The central tendency of the distribution based solely on the sampling evidence is slightly less compared with the model distribution's central tendency. Nevertheless, the difference in means from the two distributions is negligible (0.35% vs. 0.36%).

Figure A-2 shows a similar relationship for the high prevalence season. The FSIS sampling evidence and the distribution predicted by the model overlap considerably. The means of the two distributions are also very similar (0.96% for the FSIS sampling evidence and 0.94% for the model distribution).

Differences observed between the two distributions are primarily a result of the fabrication algorithm wherein half-log increments are added to grinder concentrations. Half-log increments were chosen primarily for convenience but can result in substantial shifts in the modeled values. More precise overlap between the sampling evidence and model might be achieved by using more refined increments. Furthermore, the model output is based on a set of 100 feasible simulations. More simulations would also refine the model's distribution.

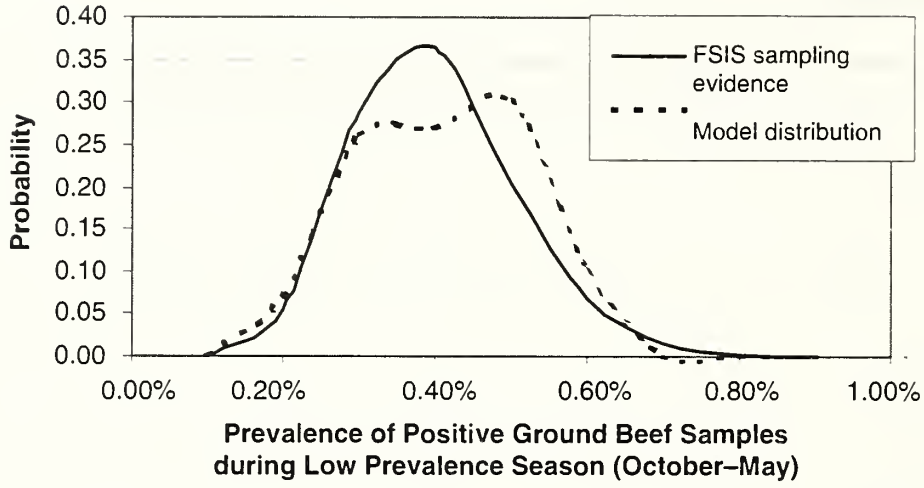

FIGURE A-1 Comparison of probability distributions for apparent prevalence of *E. coli* O157:H7-contaminated grinder loads using the FSIS sampling evidence (Table A-1) and the risk assessment model. These distributions are based on sampling evidence and model simulations for the low prevalence season.

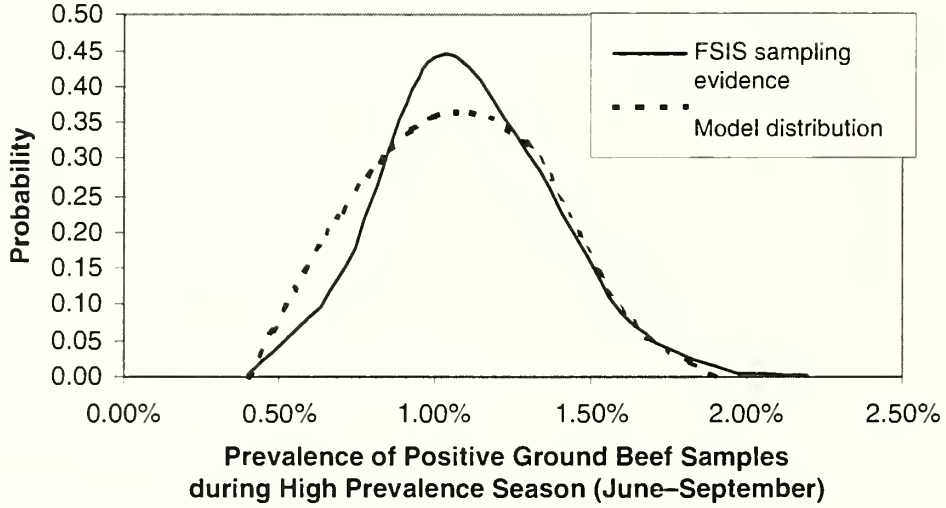

FIGURE A-2 Comparison of probability distributions for apparent prevalence of *E. coli* O157:H7-contaminated grinder loads using the FSIS sampling evidence (Table A-1) and the risk assessment model. These distributions are based on sampling evidence and model simulations for the high prevalence season.

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Appendix B

Summary of Human Clinical Trials of Foodborne Pathogens

Potential Surrogate Pathogens for *E. coli* O157:H7 (strain or serotype)	Number of Dose Groups	Total Number of Human Volunteers	Lowest Dose Tested and with Illness	Reference
1. *S. dysenteriae* (M131)[a]	4	30[b]	10, 10	Levine et al. 1973
2. *S. dysenteriae* (A-1)[c]	2	10	$2x10^2$, $2x10^2$	Levine et al. 1973
3. *S. flexneri* (2457T)[d]	5	43	10^4, 10^4	DuPont et al. 1969
4. *S. flexneri* (2457T)	4	197	10^5, 10^5	DuPont et al. 1972
5. *S. sonnei* (53G)[e]	1	20, 38	500, 500	DuPont et al. 1989
6. Enteropathogenic *E. coli* wild type (O111:NM, B1718)[f] + bicarbonate	3	13[g]	$5x10^8$, $5x10^8$	Bieber et al. 1998
7. Enteropathogenic *E. coli* (O142:H6)[h] + bicarbonate	3	15[i]	10^6, 10^6	Levine et al. 1978
8. Enteropathogenic *E. coli* (O128:H6)[j] + bicarbonate	3	15	Avirulent at 10^{6-10}	Levine et al. 1978
9. Enteropathogenic *E. coli* (O127:H6)[k] + bicarbonate	2	9	10^6, 10^{10}	Levine et al. 1978
10. Enterotoxigenic *E. coli* (O78:H11)[l] + bicarbonate	2	14[m]	10^6, 10^6	Evans et al. 1978
11. Enterotoxigenic *E. coli* (non-typable)[n]	3	14[o]	10^6, 10^8	Levine et al. 1977
12. Enterotoxigenic *E. coli* (O148:H28)[p]	2	17[q]	10^6, 10^6	Levine et al. 1979
13. Enterotoxigenic *E. coli* (O25:NM)[r]	1	6[o]	10^9, 10^9	Levine et al. 1979

Potential Surrogate Pathogens for *E. coli* O157:H7 (strain or serotype)	Number of Dose Groups	Total Number of Human Volunteers	Lowest Dose Tested and with Illness	Reference
14. Infant diarrheal *E. coli* (O111, B4, H)	4	46[s]	10^6, 10^6	June et al. 1953
15. Infant diarrheal *E. coli* (O111, B4, H)	4	46[s]	10^8, 10^8	June et al. 1953
16. Infant diarrheal *E. coli* (O111, B5)	1	1[t]	10^8, 10^8	Ferguson and June 1952, citing Neter 1950
17. Infant diarrheal *E. coli* (O111, B5)	1	6	10^9, 10^9	Ferguson and June 1952, citing Kirby 1950
18. Infant diarrheal *E. coli* (O111, B5)	1	3	Avirulent at 10^{10}	Ferguson and June 1952, citing Kirby 1950
19. Commensal *E. coli*	2	19	Avirulent at ~10^{10}	June et al. 1953
20. Commensal *E. coli*[u] + bicarbonate	1	4	Avirulent at 10^{10}	Levine et al. 1978

[a]Isolated from feces of patient in Guatemala with severe dysentery from 1970 pandemic and administered in milk.

[b]Fasting male prison volunteers.

[c]Isolated from feces of patient in Guatemala with mild dysentery and administered in milk.

[d]Isolated from feces of patient in Japan and administered in milk.

[e]Isolated from feces of 5-year-old patient in Japan and administered in milk.

[f]Isolated and administered in phosphate buffered saline with sodium bicarbonate.

[g]Fasting volunteers, 18 to 48 years of age.

[h]Isolate infant diarrheal strain from UK hospitals (Glasgow, E851/71) and administered with bicarbonate in saline; virulent at each of 3 doses administered.

[i]Healthy adult volunteers, mean age 24 years, 90-minute fast pre- and post-treatment.

[j]Isolate infant diarrheal strain from UK hospitals (Teesside, E74/68) and administered with bicarbonate in saline; avirulent in 15 healthy adults tested.

[k]Isolate infant diarrheal strain from UK residential nursery (Taunton, E2348/69) and administered with bicarbonate in saline; virulent at 1 of 2 doses administered.

[l]Isolated from severe non-Vibrio cholera case in Bangladesh.

[m]Male and female student volunteers, mean age 23.

[n]Isolated from physician traveling in Mexico with traveler's diarrhea and administered in milk with 2.5 hour fast intervals before and after treatment.

[o]Student volunteers, 18 to 29 years of age.

[p]Isolated from U.S. soldier in Vietnam with diarrhea and administered with bicarbonate in buffer.

[q]Healthy adult volunteers, mostly students, mean age 25, range 18 to 41 years of age.

[r]Isolated from physician traveling in Mexico with traveler's diarrhea and administered in milk with 2.5 hour fast intervals before and after treatment.

[s]Presumably fasting male prison volunteers, 16 to 48 years of age.

[t]Two-month old infant administered 10^8 organisms and developed diarrhea and weight loss within 24 hours.

[u]Nonpathogenic isolate from healthy laboratory scientist, administered in bicarbonate at 10^{10} in saline; avirulent in all four volunteers.

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